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(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATETM system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library(prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACON

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun
Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 23-FEB-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.428C3

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC

ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCCTCT	CCTTACTTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCCTCC	180
CTCCTTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGC	CGCCACC CGCG	GTGGAGCTCC	AGCTTTGTG	CCCTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTCCCTGTGT	GAAATTGTTA	TCCGCTCACA	480
ATTCCACACCA	ACATACGAGC	CGGAAGCATA	AAGTGTAAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTTGCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAA ACTGTGCG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTTGC	TTTTGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCNTT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGG	GATACCCNGG	AAAAAANTTT	780
AACAAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGAA	60
TTCATGGCTG	TTGGAGCAAT	AGAACCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGG	120
CTAAAGTCTG	ATGAACCTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCAG	ATGTATTTCG	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTGACGGC	240
ACAGATGCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTCATCA	TGATCACAAC	300
AAGGAACGGG	GCTCGTTAT	CACCA GTGAG	GAGCAGGACG	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTTAA	ACACCCCCAGC	CATCCCTTCT	TTCAAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTG	TTCCCTTTAG	TGAGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTCTGT	GTGAAATTGT	TATCCGCTCA	CAATTCCCC	540
AACATACGAG	CCGGAACATA	AAGTGTAAAG	CCTGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTTGCGCTCA	CTGCCGCTT	TCCAGTCGGG	AAA ACTGTGCG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAGG	CGGTTGCNTT	TTGGGCCTCT	TCCGCTTTCC	720
TCGCTCATTG	ATCCTNGCNC	CCGGTCTTCG	GTCGCGGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTN TNCCGG	TTATCCCCAA	ACNGGGATA	CCCNGA			816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGGTGT	TAAACAGCAGAG	GTGCAGGGCG	GGGGCTCACCG	60
TCCTGCTCCT	CACTGGTGAT	AAACGAGCCC	CGTTCTTGT	TGTGATCATG	ATGAACAAACC	120

TCCTCAAAAG TCAGAACCGG AGTCACACAG GCATCTGTGC CGTCAAAGAT TTGACACCAC	180
TCTGCCCTCG TCTTCTTTC AAATACATCT GCAAACCTCT TCTTCATTTC TGCCAATCA	240
TCCATGCTCA TCTGATTGGG AAGTCATCA GACTTTAGTC CANNTCCCTT GATCAGCAGC	300
TCGTAGAACT GGGGTTCTAT TGCTCCAACA GCCATGAATT CCCCATCTGC TGTCCGTAA	360
GTCGTATAGA AAGGTGCTCC ACCATCCAAC ATGTTCTGTG CTCGAGGGGG GGCCCGGTAC	420
CCAATTCGCC CTATANTGAG TCGTATTACG CGCGCTCACT GGCGTCGTT TTACAACGTC	480
GTGACTGGGA AAACCCCTGGG CGTTACCAAC TTAATCGCT TGCAGCACAT CCCCCCTTCG	540
CCAGCTGGGC GTAATANCGA AAAGGCCCGC ACCGATCGCC CTTCCAACAG TTGCGCACCT	600
GAATGGNAA ATGGGACCCC CCTGTTACCG CGCATTNAAC CCCCNGGG TTTNGTTGTT	660
ACCCCCACNT NNACCGCTTA CACTTGCCA GCGCCTTANC GCGCTCTCC TTTNCCTTT	720
CTTCCCTTCC TTTCNCCNN CTTTCCCCCG GGGTTCCCC CNTCAAACCC CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCGTGAGT CCTACTGACC TGTGCTTTCT GGTGTGGAGT CCAGGGCTGC TAGGAAAAGG	60
AATGGGCAGA CACAGGTGTA TGCCAATGTT TCTGAAATGG GTATAATTTC GTCTCTCCT	120
TCGGAACACT GGCTGTCTCT GAAGACTTCT CGCTCAGTTT CAGTGAGGAC ACACACAAAG	180
ACGTGGGTGA CCATGTTGTT TGTGGGTGC AGAGATGGGA GGGGTGGGGC CCACCCCTGGA	240
AGAGTGGACA GTGACACAAAG GTGGACACTC TCTACAGATC ACTGAGGATA AGCTGGAGCC	300
ACAATGCATG AGGCACACAC ACAGCAAGGA TGACNCTGTA AACATAGCCC ACGCTGTCCT	360
GNGGGCACTG GGAAGCCTAN ATNAGGCCGT GAGCANAAG AAGGGGAGGA TCCACTAGTT	420
CTANAGCGGC CGCCACCGCG GTGGANCTCC ANCTTTGTT CCCTTAGTG AGGGTTAATT	480
GCGCCCTTGG CNTAATCATG GTCATANCTN TTTCTGTGT GAAATTGTTA TCCGCTCACA	540
ATTCCACACA ACATACGANC CGGAAACATA AANTGTAAAC CTGGGGTGC TAATGANTGA	600
CTAACTCACA TTAATTGCGT TGCGCTCACT GCCCCTTTC CAATCNGAA ACCTGTCTTG	660
CCNCTTGCAT TNATGAATCN GCGAACCCCC GGGGAAAAGC GTTTCGTT TGGCGCTCT	720
TCCGCTTCCCT CNCTCANTTA NTCCCTNCNC TCGGTCAATT CCGCTGCNGC AAACCGGTTC	780
ACCNCTCCA AAGGGGTAT TCCGGTTCC CCNAATCCGG GGANANCC	828

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT TTTTTACTGA TAGATGGAAT TTATTAAGCT TTTCACATGT GATAGCACAT	60
AGTTTTAATT GCATCCAAAG TACTAACAAA AACTCTAGCA ATCAAGAATG GCAGCATGTT	120
ATTTTATAAC AATCAACACC TGTGGCTTT AAAATTGGT TTTCATAAGA TAATTTATAAC	180
TGAAGTAAAT CTAGCCATGC TTTTAAAAAA TGCTTTAGGT CACTCCAAGC TTGGCAGTTA	240

ACATTTGGCA TAAACAATAA TAAAACAATC ACAATTAAAT AAATAACAAA TACAACATTG	300
TAGGCCATAA TCATATAACAG TATAAGGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG	360
AATAGAACATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTACAC TCAGCCCTGA	420
CATTCAAGTTT TCAAAGTAGG AGACAGGTTC TACAGTATCA TTTTACAGTT TCCAACACAT	480
TGAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAAATG CATTACATCC TCAAGAGTTA	540
TCACCAACCC CTCAGTTATA AAAAATTTTC AAGTTATATT AGTCATATAA CTTGGTGTGC	600
TTATTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAAC AATGGTCCCC TAATGTGATT	660
GATATTGGTC ATTTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTGA ACTGGAACAT	720
TGNATNACAG TGTTCCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA	780
TGTTATTTG TTAAAAAATTA AATTTAACC TGGTGGAAAA ATAATTGAA ATNA	834

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT AAGACCCTCA TCAATAGATG GAGACATACA GAAATAGTCA	60
AACCACATCT ACAAAATGCC AGTATCAGGC GGCGGCTTCG AAGCCAAAGT GATGTTTGGA	120
TGTAAAGTGA AATATTAGTT GGCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT	180
GACGTGAAGT CCGTGGAAAGC CTGTGGCTAC AAAAATGTT GAGCCGTAGA TGCCGTCGGA	240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGTAGG AGGGTAAAT AGAGACCCAG	300
TAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTCTA TTAGACTATG	360
GTGAGCTCAG GTGATTGATA CTCCTGATGC GAGTAATACG GATGTGTTA GGAGTGGGAC	420
TTCTAGGGGA TTTAGCGGGG TGATGCCGTG TGGGGGCCAG TGCCCTCCTA GTTGGGGGGT	480
AGGGGCTAGG CTGGAGTGGT AAAAGCTCA GAAAATCCT GCGAAGAAAA AAACCTCTGA	540
GGTAATAAAAT AGGATTATCC CGTATCGAAG GCCTTTTG ACAGGTGGTG TGTGGTGGC	600
TTGGTATGTG CTTCTCGTG TTACATCGCG CCATCATTGG TATATGGTTA GTGTGTTGGG	660
TTANTANGGC CTANTATGAA GAACTTTGG ANTGAATTA AATCAATNGC TTGGCCGGAA	720
GTCATTANGA NGGCTNAAAA GGCCCTGTTA NGGGTCTGGG CTNGGTTTA CCCNACCCAT	780
GGAATNCNCC CCCCGGACNA NTGNATCCCT ATTCTTAA	818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA	60
CGGGCCCTAT TTCAAAGATT TTTAGGGAA TTAATTCTAG GACGATGGGT ATGAAACTGT	120
GGTTTGTCTCC ACAGATTTCAG GAGCATTGAC CGTAGTATAC CCCCGGTCGT GTAGCGGTGA	180
AAAGTGGTTTG GTTTAGACGT CCGGGAATTG CATCTGTTTT TAAGCCTAAT GTGGGGACAG	240
CTCATGAGTG CAAGACGTCT TGTGATGTAA TTATTATACN AATGGGGCT TCAATCGGGA	300

GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC	TGGTTCTAGG AATAATGGGG	360
GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT	GTTCTCCTAG GTTCAATACC	420
ATTGGTGGCC AATTGATTTG ATGGTAAGGG GAGGGATCGT	TGAACTCGTC TGTTATGTAA	480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA	TNAATGGCGG GCANGATATT	540
TCAAACNGTC TCTANTTCCT GAAACGTCTG AAATGTTAAT	AANAATTAAN TTNNGTTATT	600
GAATNTTNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT	ANGAAAANTA ATNNNTAANGG	660
CNTTATCNTN AAAGGTNATA ACCNCTCCTA TNATCCCACC	CAATNGNATT CCCCCACNCNN	720
ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG	TGNANNCCNC CTTTGTTCC	780
CTTNANTGAN GGTTATTNC CCCTNGCNTT ATCANCC		817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC	TGCTAACGTG GGAATCGGTG	60
CATAAGGAGA ACTTTCTGCT GGCACCGCCT AGGGACAAGC	GGGAGAGCGA CTCCGAGCGT	120
CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC	AGCTGGGACA CATCCGCGAG	180
TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC	AGTGTAGCC CGTCCTGGGG	240
TGGGGTGGCCG ANGCCTGANC CGCTCTGCCT TGCTGCC	CCCTGGGGCG CCACCCCTG	300
ACCTGCCCTGG GTCCAAACAC TGAGCCTGC TGCGGACTT	CAAGGANAAC CCCCCACANGG	360
GGATTTGCT CCTANANTAA GGCTCATCTG GGCCTCGGCC	CCCCCACCTG GTTGGCCTTG	420
TCTTTGANGT GAGCCCCATG TCCATCTGGG CCACGTGCG	GACCACCTT NGGGAGTGT	480
CTCCTTACAA CCACANNATG CCCGGCTCCT CCCGGAAACC	ANTCCCANCC TGNGAAGGAT	540
CAAGNCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG	CNGTGGAAACC CNCCTTNGT	600
TCCTTTTCNT TNAGGGTTAA TNNGCCTTG GCCTTNCCAN	NGTCCTNCNC NTNTTCCNNT	660
GTTNAAATTG TTANGCNCCC NCCNNTCCCN CNNCNNCNAN	CCCGACCCNN ANNTTNNNANN	720
NCCTGGGGGT NCCNNCNGAT TGACCCNNCC NCCCTNTANT	TGCNTTNGGG NNCNNNTGCC	780
CTTCCCTCT NGGGANNCG		799

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA	GCCGGGCATG CTGTGGTTTG	60
TAANGATGAC ACTCCCAAAG GTGGTCCTGA CAGTGGCCCA	GATGGACATG GGGCTCACCT	120
CAAGGACAAG GCCACCAGGT GCGGGGGCCG AAGCCCACAT	GATCCTTAAT CTATGAGCAA	180
AATCCCTGT GGGGGCTCT CCTTGAAGTC CGCCANCAGG	GCTCAGTCTT TGGACCCANG	240
CAGGTCATGG GTTGTNGNC CAACTGGGG CCNCAACGCA	AAANGGCNCA GGGCCTCNGN	300
CACCCATCCC ANGACGCGGC TACACTNCTG GACCTCCCNC	TCCACCACTT TCATGCGCTG	360

TTCNTACCCG CGNATNTGTC CCANCTGTT CNGTGCCNAC TCCANCTTCT NGGACGTGCG	420
CTACATACGC CCGGANTCNC NCTCCCGCTT TGTCCTATC CACGTNCCAN CAACAAATT	480
CNCNTANTG CACCNATTCC CACNTTNNC AGNTTTCCNC NNCGNGCTTC CTNTAAAAG	540
GGTTGANCCC CGGAAAATNC CCCAAGGGG GGGGGCCNNG TACCCAACTN CCCCCTNATA	600
GCTGAANTCC CCATNACCCN GNCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT	660
GGGAANANCC CTCGNCCNTN CCCCCNTTAA TCCCNCCTTG CNANGNNCNT CCCCCNNNTCC	720
NCCCNNTNG GCNTNTNANN CNAAAAGGC CNNNANCAA TCTCCTNNCN CCTCANTTCG	780
CCANCCCTCG AAATCGGCCN C	801

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC	60
ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCCTCACCGG GTTCACCTTC TCAGCCCTGC	120
AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA GAAGCAGGTG TTCCTGCCA	180
AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCCTGC	240
CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT GGGTGCTGGA GGCAGTGGCC	300
TGCTCCCACC TCCACCCGCG CTCTGCGGGG CCTCTGCCTG TGATGTCTCC GTACGTGTGG	360
TGGTGGGTGA GCCCACCGAN GCCAGGGTGG TTCCGGGCCG GGGCATCTGC CTGGACCTCG	420
CCATCCTGGA TAGTGCTTCC TGCTGTCCA NGTGGCCCCA TCCCTGTTA TGGGCTCCAT	480
TGTCCAGCTC AGCCAGTCTG TCACTGCCTA TATGGTGTCT GCGCAGGCC TGGGTCTGGT	540
CCCATTTACT TTGCTACACA GGTANTATTG GACAAGAACG ANTTGCCAA ATACTCAGCG	600
TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCTGCCCT CACTGGGTCC AACTCCCCGC	660
TCCTGTTAAC CCCATGGGGC TGCCGGCTTG GCGCCAATT TCTGTTGCTG CCAAANTNAT	720
GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG	780
GGNGTTCCC	789

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 772 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC	60
TTTGTAAAT AAATAAGTTA AATATTAAA TGCCTGTGTC TCTGTGATGG CAACAGAAGG	120
ACCAACAGGC CACATCCTGA TAAAAGGTA GAGGGGGGTG GATCAGCAAA AAGACAGTGC	180
TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCCCTCA GGACTCTTCC CCTACAAATA	240
ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTGTCATCC TAGAAACTCC CATGCAAGAG	300
CTACATTAAA CGAAGCTGCA GGTTAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT	360
TATTCAAGCTC CAAAAAACCC TTCTCTAGGT GTGTCTCAAC TAGGAGGCTA GCTGTTAAC	420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAAACCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGAA	AAAAGAAAAG	GACGCCCAN	CCCCCAGCTG	TGCANCTACG	CACCTCAACA	600
GCACAGGGTG	GCAGAAAAAA	AACCACTTA	CTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGCAC	CCCNANGGGG	GTAAACAGGA	ANCNGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCCAC	CCCNAATNTT	GCTGGAAAT	TTTCCTCCC	CTAAATTNTT	TC	772

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATT	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTCGGAT	GTCATAACAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAACATGGGG	GAAAGGCACT	GTTCTCTTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCA	GGAAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGCGACCA	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCNA	AAAATCTTC	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCAC	600
CCAACAGGGG	CTGCCCCACN	CNCNNAAACGA	TGANCCNATT	GNACAAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCTGCGN	TNGTGGCTCC	TGTTCAAGGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANN	G			751

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCCTT	60
TGTGGANCCT	CAGCAGTNCC	CTCTTCAGA	ACTCANTGCC	AAGANCCCTG	AAACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCATTTT	GCTCATCTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCC	CGTGACGTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATTT	600

GAAGANTCAC CTACTTCAAA GAAAANAGTG CCTTTCCCCC ATTTCTGTTG CAATTGACAA	660
ACGTCCCCAA CACAGCCAAT TGAAAACCTG CACCCAACCC AAANGGTCC CCAACCANAA	720
ATTNAAGGG	729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT CAAAGTTGTT CTTGTTGCCA TAACAACCAC CATAGGTAAA GCGGGCGCAG	60
TGTTCGCTGA AGGGGTTGTA GTACCAGCGC GGGATGCTCT CCTTGAGAG TCCTGTGTCT	120
GGCAGGTCCA CGCAGTGCCC TTTGTCACTG GGGAAATGGA TGCGCTGGAG CTCGTCAAAG	180
CCACTCGTGT ATTTCACCA GGCAGCTCG TCCGACGCGT CGGGGAGTT GGGGGTGTCT	240
TCACACTCCA GGAAACTGTC NATGCAGCAG CCATTGCTGC AGCGGAACGT GGTGGGCTGA	300
CANGTGCCAG AGCACACTGG ATGGGCCTT TCCATGNAN GGGCCCTGNG GGAAAGTCCC	360
TGANCCCAN ANCTGCCTCT CAAANGCCCC ACCTTGACACA CCCCGACAGG CTAGAATGGA	420
ATCTTCTTCC CGAAAGGTAG TTNTTCTGT TGCCCAANCC ANCCCCNTAA ACAAACTCTT	480
GCANATCTGC TCCGNGGGGG TCNTANTACC ANCAGGGAA AAGAACCCCA GGCNGCGAAC	540
CAANCTGTT TGGATNCGAA GCNATAATCT NCTNTTCTGC TTGGTGGACA GCACCANTNA	600
CTGNNANCT TTAGNCCNTG GTCCTCNTGG GTTGNNCNTG AACCTAATCN CCNNTCAACT	660
GGGACAAGGT AANTNGCCNT CCTTTNAATT CCCNANCNTN CCCCCCTGGTT TGGGGTTTTN	720
CNCNCTCCTA CCCCAGAAAN NCCGTGTTCC CCCCCAACTA GGGGCCNAAA CCNNTTNTTC	780
CACAACCCTN CCCCCACCCAC GGGTCNGNT GGTTNG	816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG GGCAGGCATA NACTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG	60
ATGTGGAAAA CACAGATTGG CGCCTACTGC GGGGTGACAC GGATGTCAGG GTAGAGAGGA	120
AAGACCCAAA CCAGGTGGAA CTGTGGGAC TCAAGGAANG CACCTACCTG TTCCAGCTGA	180
CAGTGACTAG CTCAGACAC CCAGAGGACA CGGCCAACGT CACAGTCACT GTGCTGTCCA	240
CCAAGCAGAC AGAAGACTAC TGCCTCGCAT CCAACAANGT GGGTCGCTGC CGGGGCTCTT	300
TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCAA GAGTTCTGTT TATGGAGGCT	360
GCTTGGCAA CAAGAACAAAC TACCTCGGG AAAAGAGTG CATTCTANCC TGTCTGGGTG	420
TGCAAGGTGG GCCTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCT	480
CCATGGAAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCCACCCAG TTCCGCTGCA	540
NCAATGGCTG CTGCATCNAC ANTTCTCTNG AATTGTGACA ACACCCCCCA NTGCCCCCAA	600
CCCTCCCAAC AAAGCTTCCC TGTTNAAAAA TACNCCANTT GGCTTTNAC AACACCCGG	660
CNCCTCCNTT TTCCCCNNTN AACAAAGGGC NCTNGCNTT GAACTGCCN AACCCNGAA	720

TCTNCCNNGG AAAAANTNCC CCCCCCTGGTT CCTNNAANCC CCTCCNCNAA ANCTNCCCCC	780
CCC	783

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTCGGAT GTCATACAAA	60
AGCTGATTGA AGCAACCCCTC TACTTTTG TGCGTGCAGCT TTTGCTTGGT GCAGGGTTCA	120
TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCAGT GTTCTCTTTG	180
AAGTAGGGTG AGTCCTCAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTTC	240
ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTTT CTTGATGGCA	300
GGCACTACCA GCAACGTCAG GAAGTGCAGA GCCATTGTGG TGTACACCAA GGGGACCACA	360
GCAGCTGCAA CCTCAGCAAT GAAGATGAGG AGGAGGATGA AGAAGAACGT CNCGAGGGCA	420
CACTTGCTCT CCGCTTCTAGC ACCATAGCAG CCCANGAAAC CAAGACCAAA GACCACAACG	480
CCNGCTGCGA ATGAAAGAAA NTACCCACGT TGACAAACTG CATGGCCACT GGACGACAGT	540
TGGCCCGAAN ATCTTCAGAA AAGGGATGCC CCATCGATTG AACACCCANA TGCCCACTGC	600
CNACAGGGCT GCNCCNCNCN GAAAGAATGA GCCATTGAAG AAGGATCNTC NTGGTCTTAA	660
TGAACTGAAA CCNTGCATGG TGGCCCTGT TCAGGGCTCT TGGCAGTGAA TTCTGANAAA	720
AAGGAACNGC NTNAGCCCC CCAAANGANA AAACACCCCC GGGTGTGCG CTGAATTGGC	780
GGCCAAGGAN CCCTGCCCN G	801

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA GGCGTCCCTC TGCCTGCCCA CTCAGTGGCA ACACCCGGGA GCTGTTTGT	60
CCTTTGTGGA GCCTCAGCAG TTCCCTCTT CAGAACTCAC TGCCAAGAGC CCTGAACAGG	120
AGCCACCATG CAGTGCTTC GCTTCATTAA GACCATGATG ATCCTCTTC ATTTGCTCAT	180
CTTTCTGTGT GGTGCAGCCC TGTTGGCAGT GGGCATCTGG GTGTCAATCG ATGGGGCATC	240
CTTTCTGAAG ATCTTCGGGC CACTGTGTC CAGTGCCATG CAGTTIGTCA ACGTGGGCTA	300
CTTCCTCATC GCAGCCGGCG TTGTGGCTTT TGCTCTTGGT TTCCCTGGCT GCTATGGTGC	360
TAAGACGGAG AGCAAGTGTG CCCTCGTGC GTCCTTCTTC ATCCTCCTCC TCATCTTCAT	420
TGCTGAAGTT GCAGCTGCTG TGGTGCCTT GGTGTACACC ACAATGGCTG AACCAATTCT	480
GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAGGAA AAATTCACTC	540
AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTICCCCC AACTATACCG	600
GAATTTCGAA AGANTCNCCC TACTTCCAAA AAAAAANANT TGCCTTNCC CCCNTCTGT	660
TGCAATGAAA ACNTCCCAAN ACNGCCAATN AAAACCTGCC CNNNCAAAAA GGNTCNAAA	720
CAAAAAAANT NNAAGGGTTN	740

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATACACA GCCTCAATCA	60
CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGAAC ACTGCATATG	120
GGATACACTT TACTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT	180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCAGCTAA GTAGTCAGCG TATGTCCCCAT	240
AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA	300
CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT	360
GGATGAGTGT GGCCAGCGCT GCCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT	420
GGTTCTGCCCG TGTCAACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG	480
GCTCAGGATG TCCAGAGAGC TGTTCCGCC CCCTCNCTTA ATGACACCGN CCANNCAACC	540
GTCGGCTCCC GCCGANTGNG TTCGTCGTNC CTGGGTCAGG GTCTGCTGGC CNCTACTTGC	600
AANCTCGTC NGGCCCATGG AATTCAACCNC ACCGGAACTN GTANGATCCA CTNNNTCTAT	660
AACCGGNCGC CACCGCNNT GGAACTCCAC TCTTNTTNCC TTTACTTGAG GGTAAAGGTC	720
ACCCCTNNCG TTACCTTGCT CCAAACCTN CCNTGTGTG ANATNGTNA TCNGGNCCNA	780
TNCCANCCNC ATANGAAGCC NG	802

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC AGGTNACGGG CCGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG	60
GAGCCCACCG TCACGNNGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT	120
CNTGACCCCA ACTCCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG	180
CAGGAACCAA GANCAAANN NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG	240
GCNCATCCNT CNAGTGCTGN AAAGCCCCNN CCTGTCTACT TGTTTGAGA ACNGCENNNGA	300
CATGCCCAAGN GTTANATAAC NGGCNGAGAG TNANTTTGCC TCTCCCTTCC GGCTGCGCAN	360
CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCCT	420
CCACTAAGCT CAGAACAAAA AACTTCGACA CCACTCANTT GTCACCTGNC TGCTCAAGTA	480
AAGTGTACCC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTGG	540
GAAGACCTAT CAATTNAAGC TATGTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCNACC	600
CNNCNNTCCA AGGGGGGGNC GGCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCN	660
CCCCCNGGCC CGGCCTTTA CNANCNTCNN NNACNGGGNA AAACCNNNGC TTTNCCCAAC	720
NNAATCCNCC T	731

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT TTTTTTTTTT TAAAAACCCC CTCCATTNAA TGNAAACTTC CGAAATTGTC	60
CAACCCCCCTC NTCCAAATNN CCNTTCCGG GNNGGGGTTTC CAAACCCAAN TTANNTTTGG	120
ANNTTAAATT AAATNTTNNT TGGNGGNNA ANCCNAATGT NANGAAAGTT NAACCCANTA	180
TNANCCTNAA TNCCCTGGAAA CCNGTNGNTT CAAAAAATNT TTAACCCTTA ANTCCCTCCG	240
AAATNGTTNA NGGAAAACCC AANTTCTCNT AAGGTTGTTT GAAGGNTNAA TNAAAANCCC	300
NNCCAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTCC NTTAAAANAA	360
GGNNANCCCC GTTTANTNAA TCCCCCNNC CCCAATTATA CCGANTTTTT TTNGAATTGG	420
GANCCNCGG GAATTAACGG GGNNNNNTCCC TNTTGGGGGG CNGGNNCCCC CCCCNCTCGGG	480
GGTTNGGGNC AGGNCNNAAT TGTTTAAGGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC	540
CCAGGNTGAG NNTNGGGTTT NCCCCCCCCC CANGGCCCT CTCGNANAGT TGGGGTTTGG	600
GGGGCCTGGG ATTTTNTTTC CCCTNTTNCC TCCCCCCCCC CCNNGGANAG AGGTTNGNGT	660
TTTGNTCNNC GGCCCCNCCN AAGANCTTN CCGANTTNAN TTAAATCCNT GCCTNGGCAGA	720
AGTCCNTTGN AGGGNTAAAN GGCCCCCTNN CGGG	754

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT GACCCNAAC NNNGGACCN TCANCCGGNC NNNCNACCNC CGGCCNATCA	60
NNGTNAGNNC ACTNCNNNT NATCACNCCC CNCCNACTAC GCCCNCNANC CNACGCNCTA	120
NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAANCT NATACCANAG NCACCCANACN	180
CCAGCTGTCC NANAANGCCT NNNATACNGG NNNATCCAAT NTGNANCCTC CNAAGTATTN	240
NNCNNCANAT GATTTCCCTN ANCCGATTAC CCNTNCCCCC TANCCCTCC CCCCCAACNA	300
CGAAGGCNCT GGNCCNAAGG NNCGNCNCC CCGCTAGNTC CCCNNAAGT CNCNCNCCTA	360
AACTCANCCN NATTACNCGC TTCNTGAGTA TCACTCCCCG AATCTCACCC TACTCAACTC	420
AAAAANATCN GATACAAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCTCTATT	480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATT CCNAANGGCT	540
CTTTCNGACA GCATNTTTTG GTTCCNNNT GGGTTCTTAN NGAATTGCCC TTCNTNGAAC	600
GGGCTCNTCT TTTCCTTCGG TTANCTGGN TTCNNCCGGC CAGTTATTAT TTCCCNNTTT	660
AAATTCTNCA CNTTANTTT TGGCNTTCNA AACCCCCGGC CTTGAAAACG GCCCCCTGGT	720
AAAAGGTTGT TTTGANAAAA TTTTGTTTT GTTCC	755

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTTT TTTTTTANGTG TNGTCGTGCA GGTAGAGGCT TACTACAANT GTGAANACGT	60
ACGCTNGGAN TAANGCGACC CGANTTCTAG GANNCCNCC AAAATCANAC TGTGAAGATN	120
ATCCTGNNNA CGGAANGGTC ACCGGNNGAT NNTGCTAGGG TGNCCNCTCC CANNNCNTTN	180
CATAACTCNG NGGCCCTGCC CACCACCTTC GGCGGCCNG NGNCCCCGCG CCGGTCAATTN	240
GNNTTAAACCN CACTNNGCNA NCGGTTCCN NCCCCNNCNG ACCCNGGCGA TCCGGGGTNC	300
TCTGTCTTCC CCTGNAGNCN ANAAANTGGG CCNCGGNCCC CTTTACCCCT NNACAAGCCA	360
CNGCCNTCTA NCCNCNGCCC CCCCTCCANT NNGGGGGACT GCCNANNGCT CCGTTNCTNG	420
NNACCCNNN GGGTNCTCG GTTGTGANT CNACCGNANG CCANGGATTG CNAAGGAAGG	480
TGCGTTNTTG GCCCCATCCC TTCGCTNCGG NNCACCCCTTC CCGACNANGA NCCGCTCCCG	540
CNCNNCGNNG CCTCNCCCTCG CAACACCCGC NCTCNTCNGT NCGGNNNCCC CCCCACCCGC	600
NCCCTNCNC NGNCGNANCN CTCCNCCNCC GTCTCANNCA CCACCCCGCC CCGCCAGGCC	660
NTCANCCACN GGNNGACNNG NAGCNCNNTC GCNCNGCGCN GCGNCNCCT CGCCNCNGAA	720
CTNCNTCNGG CCANTNNCGC TCAANCCNA CNAAACGCCG CTGCGCGGCC CGNAGCGNCC	780
NCCTCCNCGA GTCCTCCCGN CTTCCNACCC ANGNNNTCCN CGAGGACACN NNACCCCGCC	840
NNCANGCGG	849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAACTA TACTTCGCTC GNACTCGTGC GCCTCGCTNC TCTTTCCCTC CGCAACCATG	60
TCTGACNANC CCGATTNGGC NGATATCNAN AAGNTCGANC AGTCAAACACT GANTAAACACA	120
CACACNCNAN AGANAAATCC NCTGCCTTCC ANAGTANACN ATTGAACNNG AGAACCCANGC	180
NGGCGAATCG TAATNAGGG TGCGCCGCCA ATNTGTCNCC GTTTATTNTN CCAGCNTCNC	240
CTNCCNACCC TACNTCTTCN NAGCTGTCNN ACCCCTNGTN CGNACCCCCC NAGGTGGGA	300
TCGGGTTTNN NNTGACCGNG CNNCCCTCC CCCCNCTCCAT NACGANCCNC CGGCACCAACC	360
NANNGCNCGC NCCCCGNNCN CTTGCCNCC CTGCTCTNTN CCCCTGTNGC CTGGCNCNGN	420
ACCGCATTGA CCCTCGCCNN CTNCNGAAA NCGNANACGT CCGGGTTGNN ANNANCCTG	480
TGGGNNNGCG TCTGCNCCGC GTTCCTTCCN NONNCTTCCA CCATCTTCNT TACNGGGTCT	540
CCNCGCCNTC TCNNNCACNC CCTGGGACGC TNTCCTNTGC CCCCTTNAC TCCCCCCCCTT	600
CGNCGTGNCC CGNCCCCACC NTCATTNCA NACGNTCTTC ACAANNNCCT GGNTNNCTCC	660
CNANCNGNCN GTCANCCNAG GGAAGGGNGG GGNCCNNTG NTTGACGTTG NGNGANGTC	720
CGAANANTCC TCNCCNTCAN CNCTACCCCT CGGGCGNNCT CTCNGTTNCC AACTTANCAA	780
NTCTCCCCCG NGNGCNCNTC TCAGCCTCNC CCNCCCCNCT CTCTGCANTG TNCTCTGCTC	840
TNACCNNTAC GANTNTTCGN CNCCCTCTT CC	872

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC TTGAGTATTTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA	60
NCTGNCTTCC TGTGTCAAAT GTATACNAAN TANATATGAA TCTNATNTGA CAAGANNGTA	120
TCNTNCATTA GTAACAANTG TNNTGTCCAT CCTGTCNGAN CANATTCCC A TNNATTNCGN	180
CGCATTNCNC GCNCANTATN TAATNNGGAA NTCNNNTNNN NCACNNNCAT CTATCNTNC	240
GCNCCTGAC TGGNAGAGAT GGATNANTTC TNNTNTGACC NACATGTTCA TCTTGGATTN	300
AANANCCCC CGCNGNCCAC CGGTTNGNNG CNAGCCNNTC CCAAGACCTC CTGTGGAGGT	360
AACCTGCGTC AGANNCATCA AACNTGGAA ACCCGCNMCC ANGTONNAAGT NGNNNCANAN	420
GATCCCGTCC AGGNTTNAACC ATCCCTTCNC AGCGCCCCCT TTNGTGCCTT ANAGNGNAGC	480
GTGTCNNANC CNCTCAACAT GANACCGGCC AGNCCANCCG CAATTNGGCA CAATGTCNC	540
GAACCCCCCTA GGGGGANTNA TNCAAANCCC CAGGATTGTC CNCNCANGAA ATCCCNCANC	600
CCCNCCCTAC CCNNCTTGG GACNGTGACC AANTCCCGGA GTNCCAGTCC GGCCNGNCTC	660
CCCCACCGGT NNCCNTGGGG GGGTGAANCT CNGNNTCANC CNGNCGAGGN NTCGNAAGGA	720
ACCGGNCTN GGNCGAANNG ANCNCNTNGA AGNGCCNCNT CGTATAACCC CCCCTCNCCA	780
NCCNACNGNT AGNTCCCCCCC CNGGGTNCGG AANGG	815

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGCGCT ACTCTCTCTT TCTGGCCTGG	60
AGGCTATCCA GCGTACTCCA AAGATTCAAGG TTTACTCAGG TCATCCAGCA GAGAATGGAA	120
AGTCAAATTTC CCTGAATTGC TATGTGTCTG GGTTTCATCC ATCCGACATT GAANTTGACT	180
TACTGAAGAA TGGANAGAGA ATTGAAAAAG TGGAGCATTC AGACTTGTCT TTCAGCAAGG	240
ACTGGTCTTT CTATCTCNGT TACTACACTG AATTCAACCC CACTGAAAAA GATGAGTATG	300
CCTGCCGTGT GAACCAGTGTG ACTTTGTCAC AGCCCAAGAT AGTTAAGTGG GATCGAGACA	360
TGTAAGCAGN CNNCATGGAA GTTTGAAGAT GCCGCATTG GATTGGATGA ATTCAAATT	420
CTGCTTGCCTT GCNTTTAAAT ANTGATATGC NTATACACCC TACCCCTTAT GNCCCCAAAT	480
TGTAGGGGTT ACATNANTGT TCNCNTNGGA CATGATCTTC CTTTATAANT CCNCCNTTCG	540
AATTGCCCGT CNCCCNGTNN NGAATGTTTC CNNAACCACG GTTGGCTCCC CCAGGTCNCC	600
TCTTACGGAA GGGCCTGGGC CNCTTNCAA GTTGGGGGA ACCNAAAATT TCNCTNTGC	660
CCNCCCNCCA CNNTCTTGNG NNCNCANTTT GGAACCCCTTC CNATTCCCT TGGCCTCNNA	720
NCCTTNCTA ANAAAACCTTN AAANGTNGC NAAANNTTN ACTTCCCCCCC TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC AGTGTAAATCT TTTCCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT	60
CCCANAGATA NCTTATANCA ACAGTGCTTT GACCAAGAGC TGCTGGCAC ATTTCCTGCA	120
GAAAAGGTGG CGGTCCCCAT CACTCCTCCT CTCCCCTAGC CATCCCAGAG GGGTGAGTAG	180
CCATCANGCC TTCCGGTGGGA GGGAGTCANG GAAACAACAN ACCACAGAGC ANACAGACCA	240
NTGATGACCA TGGGCGGGAG CGAGGCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA	300
NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGCACCC	360
TTCCTACCTG ACNACCAGNG ACCNNNAACT GCNGCCTGGG GACAGCNCTG GGANCAGCTA	420
ACNNAGCACT CACCTGCCCT CCCATGGCCG TNCGCNTCCC TGGTCCTGNC AAGGGAAGCT	480
CCCTGTTGGA ATTNCGGGGA NACCAAGGGGA NCCCCCTCTT CCANCTGTGA AGGAAAAANN	540
GATGGAATTT TNCCCTTCCG GCCNNNTCCC TCTTCCTTTA CACGCCCCCT NNTACTCNCT	600
TCCCTCTNTT NTCCTGNNCNC ACTTTTNACC CCNNNATTTC CCTTNATTGA TC GGANNCTN	660
GANATTCCAC TNNGCCTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGGAT	720
GGGNNCCTCG NTCATCCTCT CTTTTCNCT ACCNCNNNTT CTTTGCCCTC CCTTNGATCA	780
TCCAACCNTC GNTGGCCNTN CCCCCCENN TCCCTTNCCC	820

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT GGCCCTTTCC TCCTCAGGGGA CCTCTGACTG CTCTGGGCCA AAGAATCTCT	60
TGTTTCTTCT CCGAGCCCCA GGCAGCGGTG ATTCAAGCCCT GCCCCAACCTG ATTCTGATGA	120
CTGCGGATGC TGTGACGGAC CCAAGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGGGCGC	180
CTGCTGAGCA CTTCCGCCCT TCACCCCTGCC CAGCCCCCTGC CATGAGCTCT GGGCTGGGTC	240
TCCGCGCTCCA GGGTTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC	300
TTCTTCCTGC CCCNTCCCTG GCTCTGANTC TCTGTCTTCC TGTCCTGTGC ANGCNCCTTG	360
GATCTCAGTT TCCCTCNCTC ANNGAACTCT GTTCTGANN TCTTCANTTA ACTNTGANTT	420
TATNACCNAN TGGNCTGTNC TGTCNNACTT TAATGGGCCN GACCGGCTAA TCCCTCCCTC	480
NCTCCCTTCC ANTTCCNNNA ACCNGCTTNC CNTCNTCTCC CCNTANCCCG CCNGGGAAANC	540
CTCCCTTGCC CTNACCANGG GCCNNNACCG CCCNTNNCTN GGGGGGCNNG GTNNCTNCNC	600
CTGNTNNNNCC CNCTCNCTN TNCCCTCGTCC CNNCNNCGCN NNGCANNTTC NCNGTCCNN	660
TNNCTCTTCN NGTNTCGNAA NGNTNCNTN TNNNNNGNCN NGNTNTNCN TCCCTCTCNC	720
CNNNTGNANG TNNTTNNNNC NCNGNNCCCN NNNNCNNNNN NGNNNTNNN TCTNCNCNGC	780
CCCNCCCCC NGNATTAAGG CCTCCNNCTC CCGGCCNC	818

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG GAGGGATATT GTANGGGATT GAGGGATAGG AGNATAANGG GGGAGGTGTG	60
TCCCAACATG ANGGTGNNGT TCTCTTTGA ANGAGGGTTG NGTTTTANN CCNGGTGGGT	120
GATTNAACCC CATTGTATGG AGNAAAAGGN TTTNAGGGAT TTTTCGGCTC TTATCAGTAT	180
NTANATTCCCT GTNAATCGGA AAATNATNTT TCNNCNGGAA AATNTTGCTC CCATCCGNA	240
ATTNCTCCCG GGTAGTGCAT NTTNGGGGN CNGCCANGTT TCCCAGGCTG CTANAATCGT	300
ACTAAAGNTT NAAGTGGGAN TNCAAATGAA AACCTNNCAC AGAGNATCCN TACCCGACTG	360
TNNNTTNCCCT TCGCCCTNTG ACTCTGCNNG AGCCCAATAC CCNNNGNGNAT GTCNCCCN	420
NNNGCGNCNC TGAAANNNNC TCGNGGCTNN GANCATCANG GGGTTTCGCA TCAAAAGCNN	480
CGTTTCNCAT NAAGGCACCT TNGCCTCATC CAACCNCNTNG CCCTCNCCCA TTTNGCCGTC	540
NGGTTCNCCCT ACGCTNNNTG CNCCCTNNNTN GANATTTNC CCGCCTNGGG NAANCCTCCT	600
GNAATGGTA GGGNCTTNTC TTTTNACCNN GNGGTNTACT AATCNCTNC ACGCNTNCTT	660
TCTCNACCCCC CCCCTTTT CAATCCCANC GGCNAATGGG GTCTCCCCNN CGANGGGGG	720
NNNCCCANNC C	731

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGNCNC TTCTATGANT ANTNTTAGAT	60
CGCTCANACC TCACANCCCTC CCNACNANGC CTATAANGAA NANNAATAGA NCTGTNCNN	120
ATNTNTACNC TCATANNCCCT CNNNNACCCAC TCCCTCTTAA CCCNTACTGT GCCTATNGCN	180
TNNCTANTCT NTGCCGCCTN CNANCCACCN GTGGGCCNAC CNCNNGNATT CTCNATCTCC	240
TCNCCATNTN GCCTANANTA NGTNCATACC CTATACCTAC NCCAATGCTA NNNCTAACNC	300
TCCATNANTT ANNNTAACTA CCACTGACNT NGACTTTCNC ATNANCTCCT ATTTGAATC	360
TACTCTGACT CCCACNGCCT ANNNATTAGC ANCNTCCCCC NACNATNTCT CAACCAAATC	420
NTCAACAACC TATCTANCTG TTCNCCAACC NTTNCCTCCG ATCCCCNNAC AACCCCCCTC	480
CCAAATAACCC NCCACCTGAC NCCTAACCCN CACCATCCCG GCAAGCCNAN GGNCATTAN	540
CCACTGGAAT CACNATNGGA NAAAAAAAAC CCNAACTCTC TANCNNAT CTCCCTAANA	600
AATNCTCTN NAATTTACTN NCANTNCCAT CAANCCACN TGAAACNNAA CCCCTGTTT	660
TANATCCCTT CTTTCGAAAA CCNACCCCTT ANNNCCCAAC CTTTNGGGCC CCCCCNCTNC	720
CCNAATGAAG GNCNCCCAAT CNANGAAACG NCCNTGAAAA ANCNAAGGCNA ANANNNTCCG	780
CANATCCTAT CCCTTANTTN GGGGNCCCTT NCCCNGGGCC CC	822

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCATT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCTT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTTGT	420
TCCCNNTAAC	GAAGGTTAAC	TGCNCCTTG	GCGTAATCAT	NGGTCANAAC	TNTTTCTGT	480
GTGAAATTGT	TINTCCCTC	NCNATTCCNC	NCNACATACN	AACCCGGAAN	CATAAAAGTGT	540
TAAAGCCTGG	GGGTNGCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTCCN	TTCNGGAAA	CTGTCNTCCC	CTGCNTTNNT	GAATCGGCCA	CCCCCCNGGG	660
AAAAGCGGTT	TGCNTTTNG	GGGGNTCCTT	CCNCTCCCC	CCTCNCTAAC	CCCTNCGCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCCNC	NAAGGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGTGGGG	GTGTGTGTAC	60
CATGTACCAAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AAACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNCACANATC	CCTACGATT	TTGACACCTG	GATTTCACCA	300
GGGGACCTTC	TGTTCTCCCA	NGGNACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCCACCTCT	CCNCNTAAC	AAAGTAATTCA	CCCCCCCCCN	CCNTCTNTTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAAC	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTTNNCNT	CANCTAATGC	CCCCCNGGC	AACNATCCAA	TCCCCCCCCN	TGGGGGCCCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNCCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCCC	CCNNCGNNG					799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTNTCCNAG	GGCAGGTTA	TTGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGCG	GCGGCGGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTN	AATTCCACG	GCGACAATGC	GGTCGCANCC	CCTCACCCACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCCNCCG	TTGGCNCACT	CCCCNTGGAA	ACCACTTNTC	360
GCGGCTCCGG	CATCTGGTCT	AAACACCTGC	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	AAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCN	AAAAAAANC	CCGGGGGGNC	CCAGTTCAA	CAAAGTCATC	600
CCCCCTGGCC	CCCAAATCCT	CCCCCCGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNNGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCCC	NNGNNAACGNC	TANCAANGNA	TCCCTTTTTT	TANAAACGGG	780
CCCCCCNCG						789

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCAATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACCT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTGTC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTTGAGGA	GGTTGTTCAT	CATGATCACA	300
ACAANGAACG	GGGCTCGTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCC	GCCATCCCTT	CTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTT	GTTCCCTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTCCCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCCGAACG	ATNAAATTTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCCCT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTG	CTTNTTGGGG	720
CGCNCCTCCC	GCTTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTCGG	CTTGCAGGCNA	780
ACGGTATCNA	CCT					793

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGGGA	ACCGTAAAAG	CCCCAATCTT	60
ANCAAGTGCG	GGGAANAGCT	GGGTGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAAACAG	CAGCTAATTG	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCCGT	CTGTCCCAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCCCTGGA	GCAATACTGA	TGGANGGCAG	CTACCNAAA	GTNTTCCCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAATCG	GCCCCGCCATC	GGGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTTGA	720
AATTNTTAAC	CCCCCACAAT	TCCACGCCNA	CATTNG			756

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGA	GCTCTGGCT	GCTGTNTTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATTT	CACCTCCAAT	180
AATCTCNGG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGACCTC	CCCTTCAAAG	TTGTTCCGGC	CTTCATCAA	300
CTTCTNNAAN	ANGANNANCC	CANCTTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCCTCTGC	TGCCTGCAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCN	TCCTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNTCCNN	CAGGGTTGGT	GGCANNCGG	GCCCNTGCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGGG	600
GGAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNTCN	CCTCGGGCCA	TTCTGGATTT	720
NCCNAACTTT	TTCTTCCCC	CNCCCCNCGG	NGTTGGNTT	TTTCATNGGG	CCCCAACTCT	780
GCTNTGGCC	ANTCCCTGG	GGGCNTNTAN	CNCCCCCTNT	GGTCCCNNTNG	GGCC	834

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCC GTTCCA	TGACNAAGGC	TCC CTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGT	180
GGAAAGGCCT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTACT	240
AATGGAAAAA	AAAATAAAC	AANAGGTTT	GTTCTCATGG	CTGCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAATATT	CTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTCCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNCACTG	GATCTGCCA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCCCTGAAC	GANATGCTTC	CANCANCCCT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCT	GGGTCCCANT	CCCTCCTT	TTNCTTACGT	660
TGTNTGGAC	CCNTGCTNGN	ATNACCAAN	TGANATCCCC	NGAAGCACCC	TNCCCTGGC	720
ATTTGANNTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGNCNCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAACCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTTGTTAGTAC	CAGCGCGGGG	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTG	TCACTGGGG	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTGTCAC	ACTCCACTAA	ACTGTCGATN	CANCAGCCCA	TTGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTTCCA	TGGAAGGGCC	TGGGGAAAT	360
CNCCTNANCC	CAAAC TGCC	CTCAAAGGCC	ACCTTGACACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGAAAATC	TGCTCCGTGG	GGGTCA	TACCA	GGGAAANAA	ACCCGGCNGN	540
GANCCNCC	CTTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTT	TGGAANAGCA	600
CAATGAACT	GTAAACNTT	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAA	GGTANGTGCC	TTCCTGAA	TCCCAAANTT	CCCCTNGNTT	TGGGTNNNTT	720
CTCCTCTNCC	CTAAAATCG	TNTTCCCCC	CCNTANGGCG			760

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTAAAAAA	CCCCCTCCAT	TGAATGAAAA	60
CTTCCNAAAT	TGTCCAACCC	CCTCNCCAA	ATNNCCATT	CGGGGGGGG	GTTCCAAACC	120

CAAATTAATT TTGGANTTTA AATTAAATNT TNATTNGGGG AANAANCAA ATGTNAAGAA	180
AATTTAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAA ATTNTTAACC	240
CTTAAATCCC TCCGAAATTG NTAANGAAA ACCAAATTCTN CCTAAGGCTN TTTGAAGGTT	300
NGATTAAAC CCCCTTNANT TNTTTTNACC CNNGNCTNAA NTATTNGNT TCCGGTGT	360
TCCTNTTAAN CNTNGTAAAC TCCCCTAAT GAANNNCCTT AANCCAATTA AACCGAATT	420
TTTTGAATT GGAAATTCCN NGGAATTNA CCGGGGTTTT TCCCNTTG GGGCCATNCC	480
CCCNCTTCG GGGTTGGGN NTAGGGTGA TTTTTNNANG NCCCCAAAAA NCCCCCAANA	540
AAAAAAACTCC CAAGNNTTAA TTNGAATNTC CCCCTTCCCA GGCCTTTGG GAAAGGNGGG	600
TTTNITGGGG CCNGGGANIT CNTTCCCCN TTNCNCNC CCCCCCNGGT AAANGTTAT	660
NGNNTTTGGT TTTTGGGCC CTTNANGAC CTTCCGGATN GAAATTAAAT CCCGGGNCG	720
GCG	724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTT TTTTCTTG CTCACATTAA ATTNTTATTT TGATTTTTT TAATGCTGCA	60
CAACACAATA TTTATTCAT TTGTTCTTT TATTCATTT TATTTGTTTG CTGCTGCTGT	120
TTTATTTATT TTTACTGAAA GTGAGAGGGAA ACTTTTGTGG CCTTTTTTCC TTTTCTGTA	180
GGCCGCCCTTA AGCTTTCTAA ATTGGAACA TCTAAGCAAG CTGAANGAA AAGGGGGTTT	240
CGCAAAATCA CTCGGGGAA NGGAAGGTT GCTTTGTTAA TCATGCCCTA TGTTGGGTGA	300
TTAACTGCTT GTACAATTAC NTTTCACTTT TAATTAATTG TGCTNAANGC TTAAATTANA	360
CTTGGGGGTT CCCTCCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG	420
TCCCGGCNT CNTGAAACA CACNGCNGAA NGTTCTCATT NTCCCNCCNC CAGGTNAAAA	480
TGAAGGGTTA CCATNTTTAA CNCCACCTCC ACNTGGCENN GCCTGAATCC TCNAAAANCN	540
CCCTCAANCN AAATTNCTNNG CCCCGGTCNC GCNTNNGTCC CNCCCGGGCT CCGGGAANTN	600
CACCCCNNGA ANNCNNNNC NAACNAAATT CGAAAAATAT TCCCNNTCNC TCAATTCCCC	660
CNNAGACTNT CCTCNCCNAN CNCAATTTC TTTNNNTCAC GAACNCNNC CNAAAATGN	720
NNNNCNCCCTC CNCTNGTCCN NAATCNCCAN C	751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTTT CTGTAAGATC AGGTGTTCCCT CCCTCGTAGG TTTAGAGGAA ACACCCCTCAT	60
AGATGAAAAC CCCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGGG GTAGGAGGGG	120
CGCCCTATGC ACAGCTGGGG CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA	180
TGGTCTGGAA GCGGCGGCTG TACCTGCGTA GGGGCACACC GTCAGGGCCC ACCAGGAACT	240
TCTCAAAGTT CCAGGCAACN TCGTTGCGAC ACACCGGAGA CCAGGTGATN AGCTTGGGT	300

CGGTCTATAAN CGCGGTGGCG TCGTCGCTGG GAGCTGGCAG GGCCTCCGC AGGAAGGCNA	360
ATAAAAGGTG CGCCCCCGCA CCGTTCANCT CGCACTTCTC NAANACCAG ANGTTGGGCT	420
CNAACCCACC ACCANNCCGG ACTTCCTTGA NGGAATTCCC AAATCTCTTC GNTCTTGGC	480
TTCTNCTGAT GCCCTANCTG GTTGCCNGN ATGCCAANCA NCCCCAANCC CCGGGGTCT	540
AAANCACCCN CCTCCTCNNT TCATCTGGGT TNTNTTCCCC GGACCNNTGGT TCCTCTCAAG	600
GGANCCCATA TCTCNACCAN TACTCACCN NCCCCCCNT GNNACCCANC CTTCTANNGN	660
TTCCCNCCCC NCCTCTGGCC CNTCAAANAN GCTTNCACNA CCTGGGTCTG CCTTCCCCCC	720
TNCCCTATCT GNACCCCN CN TTTGTCTCAN TNT	753

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA TCACAACAGA CATGCTTCAT CCCATAGACT TCTTGACATA GCTTCAAATG	60
AGTGAACCCA TCCCTGATTT ATATACATAT ATGTTCTAG TATTTTGGGA GCCTTTCCAC	120
TTCTTTAACCT CTGTTTCATT ATGAACACTG AAAATAGGAA TTTGTGAAGA GTAAAAAAAGT	180
TATAGCTTGT TTACGTAGTA AGTTTTGAA GTCTACATTC AATCCAGACA CTTAGITGAG	240
TGTTAAACTG TGATTTTAA AAAATATCAT TTGAGAATAT TCTTTCAGAG GTATTTTCAT	300
TTTTACTTTTG TGATTAATTG TGTTTATAT ATTAGGGTAG T	341

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA TTAGTTCTG TGCTCTTCCT TATTTAGTGT TGTATCATAA ATACTTTGAT	60
GTTTCAAACA TTCTAAATAA ATAATTTCAT GTGGCTTCAT A	101

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTCCTG GTCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTCTAG AGTTATGTTT CAGAAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCAGTAAA GAGGACTTAA TATTTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTITGTTTCT	60
GATTATTTGG TGTGTGTTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTT	120
CTCTCCATCC TCGGGCATTIC TTCCCAAATT TATATACCAAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTC TCTTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTCA TAGGTATGC	240
TGCTGTTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTA AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTGTTA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAAGTTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTTT CCAGGTGTTA ATGATGGAAG	600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGAAACAGG TCACTACTGC	660
ACTGGCCGTT CCACCTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG	720
CCGCCCGGGT GAAACTCCTGC AAACATCATGC TGCAAAGGTG CTCGCCGTTG ATGTCGAAC	780
CNTGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGTGTC CAGGAGGTGA TGGAGCCACT	840
CCCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG	180
TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTAA CACAGTTAAA	120
AAGAAGATAA TATAATTCCA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TAAATGCGAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCCTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GTTCAAGAC	120

GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAG GGGACAAAGG CTAATCCAA	240
AACATCAAAG AAAGGAAGGT GGCGTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCcccAGG CTCCTGTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGCG	420
CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCCTTG CTCCCTGCAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTTCT GACTTGCCTG ATTACTCCAG CATCTTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAAATTN TGGCTCATT ACGAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCTT AATTACAGCT CAACGCAACT	120
TGGT	124

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCAA GCANTGT	147

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAATT AATAAAAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC	60
ATGGTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACGG GGGCCGACAC ACTTGCACGG	60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCC CACTTGGCCA	180
CCTCCCTTTT GGGACCAGCA ATGT	204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA	60
GGGTATTTTC CAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACCTCTT GTATCAATT TTTTGTTCA AAATGACTGA CTTAANTATT TTTAAATATT	240
TCANAAACAC TTCCTCAAAA ATTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA	300
ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCAACC CACCACAAAGC TTTCTGGGGC	360
ATGCAACAGT GTCTTTCTT TNCTTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT	420

CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT	480
ATCACTCTTG T	491

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA GCAGGGCTAA TTACCATAAG ATGCTATTAA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTG CTTTGATAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAAACGTT AAAAAAAAGT GTTGAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTT GGAACAGAAA GGGAAAAANC	300
AGCTTGANT TTCTTGTC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTA AATNCCAAAA CATATTCAA CTCAACACTT CTTTCCNCG	420
TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTT	480
CANT	484

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCCT CTCAAGTGCC TTTTTGTTTG T	151

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCCGGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTG GTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAC TGT	133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCCGC TGCCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTNAAG TTATTGTNAT TGTAAAATAC ATTGAATTT CTGTATACTC	60
TGATTACATA CATTTATCCT TTAAAAAAGA TGTAATCTT AATTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAACTAGTT	180
TTGACTTCTA AGTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAAGTTA TCACAAAACCT ACTCAATTTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGC ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTCAACAGT ATCCCTCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA	30
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(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTTCA AAACTGACCA TCTTTATAT TTAATGCTTC	60
CTGTATGAAT AAAAATGGTT ATGTCAAGT	89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG	60
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT	97

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCCCT TTTGATGGCA	60
GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC	120
CCAACCCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TGGGTCTATAA NATGAAATCC CAANGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA	240
GGTGCTGTTT GCTCAGGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG	360
GGCGGGGAGG AGCATGT	377

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTCC CTCAGAATTG AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG	60
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AGAACCCGTG TGCCCCTTCC CACCATATCC ACCCTCGCTC CATCTTGAA CTCAAACACG	120
AGGAACTAAC TGCACCCTGG TCCTCTCCCC AGTCCCAGT TCACCCCTCCA TCCCTCACCT	180
TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT	240
TTATATATTT TTTAATAAGA TGCACTTAT GTCATTTTT AATAAAGTCT GAAGAATTAC	300
TGTTT	305

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTTGTCC CAGCACTTTA GGAATGCTGA	60
GGTGGGACCA GCCACATCTC ATGTGCAAGA TTGCCAGCA GACATCAGGT CTGAGAGATTC	120
CCCTTTAAA AAAGGGGACT TGCTAAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC	180
TGTGCTGTGC TGGAGATTCA CTTTTGAGAG AGTTCTCCTC TGAGACCTGA TCTTAGAGG	240
CTGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTG	300
CCTCTCCCAG GGCCCCAGCC TGGCCACACC TGCTTACAGG GCACTCTCAG ATGCCCATAC	360
CATAGTTCT GTGCTAGTGG ACCGT	385

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTAA TGG	73

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGGCTC	TCACCCTCCT	CTCCTGCAGC	60
TCCAGCTTG	TGCTCTGCCT	CTGAGGAGAC	CATGGCCCAG	CATCTGAGTA	CCCTGCTGCT	120
CCTGCTGGCC	ACCCTAGCTG	TGGCCCTGGC	CTGGAGCCCC	AAGGAGGAGG	ATAGGATAAT	180
CCCGGGTGGC	ATCTATAACG	CAGACCTCAA	TGATGAGTGG	GTACAGCGTG	CCCTTCAC TT	240
CGCCATCAGC	GAGTATAACA	AGGCCACCAA	AGATGACTAC	TACAGACGTC	CGCTGCGGGT	300
ACTAAGAGCC	AGGCAACAGA	CCGTTGGGGG	GGTGAATTAC	TTCCTCGACG	TAGAGGTGGG	360
CCGAACCATA	TGTACCAAGT	CCCAGCCCAA	CTTGGACACC	TGTGCCCTCC	ATGAACAGCC	420
AGAACTGCAG	AAGAACACAGT	TGTGCTCTTT	CGAGATCTAC	GAAGTCCCT	GGGGAGAAC A	480
GAANGTCCCT	GGGTGAAATC	CAGGTGTCAA	GAAATCCTAN	GGATCTGTTG	CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA	ACAGGGGCC	TCTCAGCCCT	CCTAATGACC	TCCGGCTAG	CCATGTGATT	60
TCACTTCCAC	TCCATAACGC	TCCTCATACT	AGGCCTACTA	ACCAACACAC	TAACCATATA	120
CCAATGATGG	CGCGATGTAA	CACGAGAAAG	CACATACCAA	GGCCACCACA	CACCACCTGT	180
CCAAAAAGGC	CTTCGATACG	GGATAATCCT	ATTATTATTAC	TCAGAAGTTT	TTTTCTTCGC	240
AGGGATTTTT	CTGAGCCTTT	TACCACTCCA	GCCTAGCCCC	TACCCCCCAA	CTAGGAGGGC	300
ACTGGCCCCC	AACAGGCATC	ACCCCGCTAA	ATCCCCCTAGA	AGTCCCCTAC	CTAAACACAT	360
CCGTATTACT	CGCATCAGGA	GTATCAATCA	CCTGAGCTCA	CCATAGTCTA	ATAGAAAACA	420
ACCGAAACCA	AATTATTCAA	AGCACTGCTT	ATTACAATT	TACTGGGTCT	CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG GTACAGTGTG ATCTCAGCTT TCGAAACACA TTTTCTACAT AGATAGTACT	60
AGGTATTAAT AGATATGTAA AGAAAGAAAT CACACCATT ATAATGGTAA GATTGGTTA	120
TGTGATTTA GTGGTATTT TGCCACCCCTT ATATATGTTT TCCAAACTTT CAGCAGTGAT	180
ATTATTTCCA TAACTAAAAA AGTGAGTTTG AAAAGAAAAA TCTCCAGCAA GCATCTCATT	240
TAAATAAAGG TTGTCATCT TTAAAATAC AGCAATATGT GACTTTTAA AAAAGCTGTC	300
AAATAGGTGT GACCCTACTA ATAATTATTA GAAATACATT TAAAACATC GAGTACCTCA	360
AGTCAGTTTG CCTTGAAAAA TATCAAATAT AACTCTTAGA GAAATGTACA TAAAAGAATG	420
CTTCGTAATT TTGGAGTANG AGGITCCCTC CTCAATTITG TATTTTAAA AAGTACATGG	480
TAAAAAAAAA ATTACACAAAC AGTATATAAG GCTGTAAAAT GAAGAATTCT GCC	533

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGT	60
AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAAGAGGG ACAAGGCTAA	120
AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTTGGG TTGGCTGGAG GAGCTGTGGA	180
AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT CCTCATTTGTT ATTACANAGT	240
GAGGTTCTCT GTGTGCCAC TGGTTTGAAA ACCGTTCTNC AATAATGATA GAATAGTACA	300
CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAANAC	360
GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCTT GTCTGTTATG	420
ATTTCTCTCC ATTGCAAGNA NAAACCCGTT CTTCTAAGCA AACNCAGGTG ATGATGGCNA	480
AAATACACCC CCTCTTGAAG NACCNGGAGG A	511

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC ACTGGTGCCA GTACCAAGTAC CAATAACAGT GCCAGTGCCA GTGCCAGCAC	60
CAGTGGTGGC TTCAGTGCTG GTGCCAGCCT GACCGCCACT CTCACATTG GGCTCTTCGC	120
TGGCCTTGGT GGAGCTGGTG CCAGCACCAAG TGGCAGCTCT GGTGCCTGTG GTTTCTCCTA	180
CAAGTGAGAT TTTAGATATT GTTAATCCTG CCAGTCTTC TCTTCAAGCC AGGGTGCATC	240

CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA	300
CTCTGCATTA AATCTATTG CCATTTCTGA AAAAAAAA AAAAAAAGGG CGGCCGCTCG	360
ANTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTTGCCAGC	420
CATCTGTTGT TTGCCCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCAC	480
GTCTTTCCT AANTAAAAT	499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATT GGATTCAAGCC GCGAAGAGAT	60
TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAACT	120
TCCAGGCCA CGGCTCAAGT GAATTGAAAT ACTGCATTTA CAGTGTAGAG TAAACACATAA	180
CAITGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT CTAATCAAGA	240
AAAGAATTAC AGACTCTGAT TCTACAGTG TGATTGAATT CTAAAATGG TAATCATTAG	300
GGCTTTGAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCTTC	360
CAGTTGCTT GATATATTG TTGATATTAA GATTCTTGAC TTATATTG AATGGGTTCT	420
ACTGAAAAN GAATGATATA TTCTTGAAAGA CATCGATATA CATTTATTAA CACTCTTGAT	480
TCTACAATGT AGAAAATGAA GGAAATGCC CAAATTGTAT GGTGATAAAA GTCCCGT	537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT TGTTCAAAAG ATGCAAATGA TACACTACTG CTGCAGCTCA CAAACACCTC	60
TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA	120
CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG	180
TGGCACAAAGG AGGCCATCTT TTCCTCATCG GTTATTGTCC CTAGAACGCGT CTTCTGAGGA	240
TCTAGTTGGG CTTCTTTCT GGGTTGGGC CATTTCANTT CTCATGTGTG TACTATTCTA	300
TCATTATTGT ATAACGGTTT TCAAACCNNGT GGGCACNCAG AGAACCTCAC TCTGTAATAA	360
CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTTNT TCCAGAGCTC	420
CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACA TCCCTGN	467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG CATTGGGCC GAGATGTCTC GCTCCGTGGC CTTAGCTGTG CTCGCGCTAC	60
TCTCTCTTTC TGGCCTGGAG GCTATCCAGC GTACTCCAAA GATTCAAGGTT TACTCACGTC	120
ATCCAGCAGA GAATGGAAAG TCAAATTCC TGAATTGCTA TGTGTCTGGG TTTCATCCAT	180
CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG GAGCATTGAG	240
ACTTGTCTTT CAGCAAGGAC TGGTCTTCT ATCTCTTGTA CTACACTGAA TTCACCCCCA	300
CTGAAAAAGA TGAGTATGCC TGCCGTGTGA ACCATGTGAC TTTGTCACAG CCCAAGATNG	360
TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT	400

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC TTGGTGTTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCC CGGCGGGGGA TGCGAGGCTC GGAGCACCCCT TGCCCGGCTG TGATTGCTGC	120
CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA	180
GTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAAAA	240
AAAAAAAAAA	248

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAAC	60
TCACCCAGAC CCCGCCCTGC CGCTGCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTAA ATAAATGCCT	180
GATTAAAAAA AAAAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTGTT AGGTTTTGA GACAACCCTA GACCTAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCTT ATTCTTTATT	120
CCTCTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAAATAC AAAAAGGTAG	180
TGTGATAGTA TAAGTATCTA AGTCCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT	300
CTGTTCTTG GCTAGAAAAA ATTATAAACCA GGACTTTGTT AGTTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAA GTTGGCTAT ACATAAANTA TNAAGAAATA TGGAATTAA	420
TTCCCAGGAA TATGGGGTTC ATTTATGAAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTGTT TAATACGTTA ATATGCTTN AATNAACAAG GCNTGACTTA TTTCCAAAAAA	540
AAAAAAAAAA AA	552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTT GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCTCT TATTTTCAGA	60
GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCTGTTT	180
GCAATTACAG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA	240
AGGTAAACT TTCCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC	300

TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC	360
TCTTGGCTTT CTCATAAAA TCTCTATCCA TCTCATGTTT AATTTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAAAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAA AAAAAAA	476

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTTCTTT CTGGGGGATC TTCCTGGCTC TGCCCCTCCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACCT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGGAATAAG TCCTAGGGT GGGGGGTGTG GCAAGCCGGC CT	232

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGGGGGAGC AGAACGCTAAA GCCAAAGCCC AAGAACAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCGCCACT CTCACATTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAG TGGCAGCTCT GGTGCCIGTG GTTCTCCTA CAAGTGAGAT TTTAGATATT	240
GTAAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTG	360
CCATTCAAA AAAAAAAA AAA	383

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAGA GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAAATCT TCGGACTGTG	300
AGCCCTGATG CCTTTTGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GCGGATTGAT	360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT	420
TTTCNCATAT TTTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCCTC CTGGGGCCCA GGCGGCACC TCGCTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC	60
TNCCATCGTC ATACTGTAGG TITGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA	120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG	180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTGATG ACTTTATTGA	240
GTCGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC	300
CTATCATGCC NTTGAACGTG CCGAAGAAC ACGAGCCTTG TGTGGGGGT GNAGTCTCAC	360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACTCGC CCAGGNNGAA	420
AAAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCNT TGGTGGNNNGC GCNTNCCTTT	480
T	481

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCIGCTG AGAATTCA	60
ACTTGAAAA GCAACTTNAA GCCTGGACAC TGGTATTAAA ATTCAACATA TGCAACACTT	120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCACTCACC AGTCTGGAA TAAGGGTATG	180
CCCTATTCAAC ACCTGTTAAA AGGGCGCTAA GCATTTTGATC TTCAACATCT TTTTTTTGAA	240
CACAAGTCCG AAAAAGCAA AAGTAAACAG TTNTTAATTGTTAGCCAAT TCACTTTCTT	300
CATGGGACAG AGCCATTGAA TTAAAAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG	360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAAGACA CAACTCCTTT CATATTGGGA	420
TGTTNACNAAGTATGCT CTTACAGATG GGATGCTTTT GTGGCAATTG TG	472

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCAAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG	60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATTTTTT TACTTTGTA AAAGCTTATG	120
CCTCTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGTCTTCTG TGTAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT	240
TTTATTGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG	300
GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAAA	360

ACAGAAATTG GGTNGTATAT TGAAAANANG CATCATTNAA ACGTTTTTT TTT 413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACCTCCC CGCGTCCCCGC	60
GTCCTAGCCN ACCATGGCCG GGCCCCCTGCG CGCCCCGCTG CTCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG GCGGTGAGCC CCGCGGCCGG CTCCAGTCCC GGCAAGCCGC CGCGCCTGGT	180
GGGAGGCCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCCTGCACTG GACTTTGCCG	240
TGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC	300
CCCAANAAA TTGTTACTNG GGGTAANTAA TTCTTGGAAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAAGAA CCNAGCCAAT TNGAACAAATT NCCCCTCCAT AACAGCCCCT TTAAAAAAGG	420
GAANCANTCC TGNTCTTTTC CAAATTTT	448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTTT GAGTTTATCA	60
GTAGTGATTC TGCCAAAGTT GGTGTTGTAA CATGAGTATG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTGTAG CCTTGAAGTT	180
CTCAGTGACA AGTTNNTCT GATGCGAAGT TCTNATTCCA GTGTTTAGT CCTTGCATC	240
TTTNATGTTN AGACTTGCCT CTNTNAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAAA TAGAANNACT TCTCTGCTTN GAANATTGA ATATCTTACA TCTNAAAATN	360
AATTCTCTCC CCATANNAAA ACCCANGCCC TTGGGANAAT TTGAAAAANG GNTCCTTCNN	420
AATTCNNANA ANTCAGNTN TCATACAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTTNT	ACTGTCGGAC	TGTTCANCCA	CCAACTCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGTCTGTAA	GCNTNTTAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAG	TCACATCTTC	TAGGACCTTT	TTGGATTCAAG	TTAGTATAAG	CTCTTCCACT	180
TCCTTGTTA	AGACTTCATC	TGGTAAAGTC	TAAAGTTTG	TAGAAAGGAA	TTAATTGCT	240
CGTTCTCTAA	CAATGTCCTC	TCCTTGAAGT	ATTGGCTGA	ACAACCCACC	TNAAGTCCCT	300
TTGTGCATCC	ATTTTAAATA	TACTTAATAG	GGCATTGGTN	CACTAGGTAA	AATTCTGCAA	360
GAGTCATCTG	TCTGCAAAAG	TTGCAGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCCTTT	GACTACCGTG	TGCCAGTGCT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAA	CTGGCACTTG	NCTGGAACTA	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCAGT	300
TGTCAATACT	AACCCGCTGG	TTTGCCTCCA	TCACATTTGT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTCCCC	AGTCCGAATG	TTCACATGGC	ATATNTTACT	TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCC	NATCCCACCA	CGAAGATGCG	CTTGTTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCCTT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAACTCCACT	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAGG	ATGCCGACT	GTGCGGGACC	240
TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAGCGAAT	GANGCCCAGG	GCCTTGCCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TCGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGCCGC	ACCTCACCGA	TGCCCANTGT	GTGCGGCTCC	420
AGGAACGGCN	CCAGCGTGTC	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCTTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCCGAGCA	GCCCCAGACC	GCTGCCGCC	GAAGCTAACG	CTGCCTCTGG	CCTTCCCCCTC	120
CGCCTCAATG	CAGAACCAANT	AGTGGGAGCA	CTGTGTTTAG	AGTTAACAGT	GAACACTGTN	180
TGATTTTACT	TGGGAATTTC	CTCTGTTATA	TAGCTTTCC	CAATGCTAAT	TTCCAAACAA	240
CAACAAACAAA	ATAACATGTT	TGCCTGTTNA	GTGTATAAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAAATATAT	TATTAATAA					377

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG	GGTTAGGGTC	CAGTTCCAG	TGGAAGAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGCCCA	TTCCGGGGCT	GTTCCTCGAG	GAGGAAGGGA	AGGGGCTCTG	TGTCCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCCACACAA	300

TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACTGGCCC	360
ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG	420
TGGACTCTNG TCCCNNAAAGG GGGCAGAATC TCCAATAGAN GGANNGAACCC CTTGCTNANA	480
AAAAAAAANA AAAAAA	495

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCTGCTC	60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTC	120
TAGCTGTTT GAGTTGATTC GCACCACTGC ACCACAACTC AATATGAAAA CTATTTNACT	180
TATTATTATT CTTGTGAAA GTATACAATG AAAATTTGT TCATACTGTA TTTATCAAGT	240
ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA	300
ATCGGCAAAA TGTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCTTT GTAACTTCAC	360
TTGGITATT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA	420
TTTANTTCAN TAATTTCTTT CCTTGTGTTAC GTTAATTGTTG AAAAGAATGC AT	472

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT	60
GTGGTGAAT TTCAAAATTAT TATGTAACCTT CTACTAGTTT TACTTCTCC CCCAAGTCTT	120
TTTTAACTCA TGATTTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT	180
ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAGTGTCTT GNCGANAATG TTCTAGNTAT	240
AGCTGGATAC ATACNGTGGG AGTTCTATAA ACTCATACCT CAGTGGACT NAACCAAAAT	300
TGTGTTAGTC TCAATTCCCA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT	360
GCAGGTACTC CTCCAGAAA ACNGACAGGG CAGGCTTGCA TGAAAAAGTN ACATCTGCGT	420
TACAAAGTCT ATCTTCCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA	60
AAATAATGCT GCAAACCTAA TGTTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA	120
CAATCGCAA TCAAAACTCA CAAGTGTCA TCTGTTGTAG ATTTAGTGTA ATAAGACTTA	180
GATTGTGCTC CTCGGATAT GATTGTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT	240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT	300
GTGATTATNA AATTAATCAC AAATTTCACT TATACTGCT ATCAGCAGCT AGAAAAAACAT	360
NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG	420
TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC	479

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACTGACA ATCAGACCTA	60
TGCTAGTTCC TGTCACTCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA	180
AGTGATTCACT TTTCCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA	240
TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAGACA GAGAAATAAA GTCAGAAAAT	300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAACCTTCT CTTAAGGACT	360
TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC	420
TTTGGAAATAA TCTTGACGCT CCTGAACCTG CTCCTCTGCG A	461

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT	60
CGGCGCCTCT CGGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCC	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGC GTGCC TTGGGGTAC C	171

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TCGGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGGGC GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGG	180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCCTCGGG AAGGGCGGCC	240
CGAGAGATAAC GCAGGTGCAG GTGGCCGCC	269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT TTTGGAAC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCA GTCACCTTCC TTTGTCGTGG	120
TTGATTGGTT TGTCTTATG GGGGCGGGGT GGGGTAGGGG AAACGAAGCA AATAACATGG	180
AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT GGGGCAGTTC ACCTGGTCTG	240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTT AGAGAGTCCA	300
CTGTTCTGGA GGGAGATTAG GGTTCTTGCA CAAATCCAAC AAAATCCACT GAAAAAGTTG	360
GATGATCAGT ACGAATACCG AGGCATATTC TCATATCGGT GGCCA	405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
GGCACTTAAT	CCATTTTAT	TCACAAATTG	CTACAAATTG	AATCCCATT	TACGGTATTT	120
TCAAATCTA	AATTATTCAA	ATTAGCCAAA	TCCTTACCAA	ATAATACCCA	AAAATCAAAA	180
ATATACTCT	TTCAGCAAAC	TTGTTACATA	AATTAAAAAA	ATATATAACGG	CTGGTGTTT	240
CAAAGTACAA	TTATCTTAAAC	ACTGCAAAC	TTTAAGGAA	CTAAAATAAA	AAAAAACACT	300
CCGCAAAGGT	TAAAGGGAAC	AACAAATTCT	TTTACAACAC	CATTATAAAA	ATCATATCTC	360
AAATCTTAGG	GGAATATATA	CTTCACACGG	GATCTTAACT	TTTACTCACT	TTGTTTATTT	420
TTTAAACCA	TTGTTGGGC	CCAACACAAT	GGAATCCCCC	CTGGACTAGT		470

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTTT	TTTTTTTTGA	CCCCCTCTT	ATAAAAACA	AGTTACCATT	TTATTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATT	TTAGGAATT	GCTTAAAATC	TGCCCTAAAGT	180
GAAAATCTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAAAC	ATCCAAATT	240
ATTTTCTTG	TCTTTAAAT	TATCTAATCT	TTCCATTTT	TCCCTATTCC	AAGTCATT	300
GCTTCTCTAG	CCTCATTTC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAAA	360
AGGGAAAACA	GGAAGAGAAA	TGGCACACAA	AACAAACATT	TTATATT	CAT ATTTCTACCT	420
ACGTTAATAA	AATAGCATT	TGTGAAGCCA	GCTAAAAGA	AGGCTTAGAT	CCTTTATGT	480
CCATTTAGT	CACTAACGA	TATCAAAGTG	CCAGAATGCA	AAAGGTTGT	GAACATTTAT	540
TCAAAAGCTA	ATATAAGATA	TTTCACATAC	TCATCTTCT	G		581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT TTTTTTTTTT TTTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTTT	60
CACTCTCTAG ATAGGGCATG AAGAAAACTC ATCTTTCCAG CTTTAAAATA ACAATCAAAT	120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA	180
AGGAAATCTG TTCATTCTTC TCATTCAAT AGTTATATCA AGTACTACCT TGCAATTG	240
GAGGTTTTTC TTCTCTATT ACACATATAT TTCCATGTGA ATTGTATCA AACCTTTATT	300
TTCATGCAAA CTAGAAAATA ATGTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATT	360
CAAAACTGCT CAAATTGTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC	420
AAATCACATT TACGACAGCA ATAATAAAAC TGAAGTACCA GTTAAATATC CAAAATAATT	480
AAAGGAACAT TTTTAGCCTG GGTATAATTA GCTAATTAC CTTACAAGCA TTTATTAGAA	540
TGAATTACACA TGTTATTATT CCTAGCCCAA CACAATGG	578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT TTTTTCAGTA ATAATCAGAA CAATATTTAT TTTTATATTT AAAATTCTATA	60
GAAAAGTGCC TTACATTTAA TAAAAGTTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT	120
GTCTTGAACA CCAATATTAA TTGAGGAAA ATACACCAAA ATACATTAAG TAAATTATTT	180
AAGATCATAG AGCTTGTAAAG TGAAAAGATA AAATTTGACC TCAGAAACTC TGAGCATTAA	240
AAATCCACTA TTAGCAAATA AATTACTATG GACTTCTTGC TTTAATTG TGATGAATAT	300
GGGGTGTACAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA	360
TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTCT CTTTCTCAA TCTTTTAAGG	420
GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTTCTTTCTA TGGAAGGATT	480
AGATATGTTT CCTTGCCAA TATTAAAAAA ATAATAATGT TTACTACTAG TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT TTTTTTAGTC AAGTTCTAT TTATTATTATA ATTAAAGTCT TGGTCATTTC	60
ATTTATTAGC TCTGCAACTT ACATATTAA ATTAAAGAAA CGTTTAGAC AACTGTACAA	120
TTTATAAATG TAAGGTGCCA TTATTGAGTA ATATATTCCCT CCAAGAGTGG ATGTGTCCCT	180
TCTCCCACCA ACTAATGAAC AGAACACCA GTTTAATTATT ATTAGTAGAT ATACACTGCT	240
GCAAACGCTA ATTCTCTTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG	300
AATGCATCAC AATCTACAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CGGTGAAAAT	360
AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA	420
CCGCTTCCTC AAAGGCGCTG CCACATTGT GGCTCTTTGC ACTTGTTC AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA CTGCAGGGCA TCTCGGTCA GGAGCTGTCC GGCCTGGCCC CGGGCCCGTT	60
CTGTGCTATG GTCCTGGCTG ACTTCGGGGC GCGTGTGGTA CGCGTGGACC GGCCCGGCTC	120
CCGCTACGAC GTGAGCCGCT TGGGCGGGG CAAGCGCTCG CTAGTGTCTGG ACCTGAAGCA	180
GCCGCGGGGA GCGCCGCTGC TGCGGCGTCT GTGCAAGCGG TC GGATGTGC TGCTGGAGCC	240
CTTCCGCCGC GGTGTATGG AGAAACTCCA GCTGGGCCCA GAGATTCTGC AGCGGGAAAA	300
TCCAAGGCTT ATTATGCCA GGCTGAGTGG ATTGGCCAG TCAGGAAGCT TCTGCCGGTT	360
AGCTGGCAC GATATCAACT ATTGGCTTT GTCAAGGTGTG CTCTAAAAA TTGGCAGAAG	420
TGGTGAGAAT CGCTATGCC CGCTGAATCT CCTGGCTGAC TTTGCTGGTG GTGGCCTTAT	480
GTGTGCACTG GGCATTATAA TGGCTTTTG TGACCGACA CGCACTGACA AGGGTCAGGT	540
CATTGATGCA AATATGGTGG AAGGAACAGC ATATTAAGT TCTTTCTGT GGAAACTCA	600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT	660
CTATACGACT TACAGGACAG CAGATGGGG ATTCAATGGCT GTTGGAGCAA TAGAACCCCA	720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTTC CCAATCAGAT	780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTGCA GATGTATTTG CAAAGAAGAC	840
GAAGGCAGAG TGGTGTCAAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC	900
TTTGAGGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTGTTTA TCACCAAGTGA	960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTT AACACCCAG CCATCCCTTC	1020
TTTCAAAAGG GATCCTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAG AATTGGATT	1080
CAGCCCGAA GAGATTTATC AGCTTAACCTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA	1140
AGCTAGTCTC TAACTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG	1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCCCTA	1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA	1320
AATGGTTATC ATTAGGGCTT TTGATTATAA AAACTTGGG TACTTATACT AAATTATGGT	1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTGTTGAT ATTAAGATTC TTGACTTATA	1440
TTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATT	1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT	1560

AAAAAGTCACG TGAAACAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1620
 A 1621

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

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Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1           5           10          15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
 20          25          30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
 35          40          45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
 50          55          60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
 65          70          75          80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
 85          90          95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100         105         110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115         120         125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130         135         140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
145         150         155         160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165         170         175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180         185         190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195         200         205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210         215         220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225         230         235         240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245         250         255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
260         265         270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
275         280         285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val

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290	295	300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu		
305	310	315
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala		
325	330	335
Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu		
340	345	350
Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn		
355	360	365
Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu		
370	375	380

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACCGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCGCCCTCT	ACCTCGCCGA	CAGCTGGAAC	120
CAGTGCACC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGTAAC	ACCTGGGCCG	CACTGCTCTC	TGCAATCGACT	TCATGGTTTT	CACGGTGCAGG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCCCTCGGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGGCACCGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGA	TCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATT	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCGG	GCACCTGCGT	CTCCCAGTAT	GCCAAC	TGGTGGTGCT	GCTCCTCGTC	600
ATCTTCTGC	TCGTGGCCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCAGTTAC	660
ACATTGGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTGG	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCGCGCTG	GCCCCGCCCT	TTATCGTCAT	CTCCCACTTG	780
CGCCTCTGC	TCAGGCAATT	GTGCAGGCGA	CCCCGGAGCC	CCCAGCCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTTCTAAG	GAAGCCGAGC	GGAAGCTGCT	AACGTGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAAGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGCTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCCGCGTC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCTTG	TGCCCCCAGG	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCC	GCACCTGGTG	1260
GCCTTGTCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTCACTCT	TACAAACCAC	AGCATGCCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCG	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCTCACA	CTGGGGAAAT	AAAGCCATT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAA				1524

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATTIC	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GCCGCAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCTTAC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCAGTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTCTCA	TCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCGGA	TCCCAGGCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACIICCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCCGACCA	CTGTCGCCAG	GCCTACTCTG	TCTATGCCTT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGCTA	CCTCCTGCC	GCCATTGACT	GGGACACCAAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCAAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCC	CACTGCTGTC	CATGCCGGC	1020
CCGCTTGGCT	TTCCCGAACCC	TGGGCC	GCTTCCCCGG	CTGCACCCAGC	TGTGCTGCCG	1080
CATGCCCGC	ACCCCTGCGCC	GGCTCTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTTACA	CGGATTTCGT	GGGCGAGGGG	CTGTACCAGG	GGGTGCCAG	1200
AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCGTTCGGA	TGGGCAGCCT	1260
GGGGCTGTTG	CTGCAGTGC	CCATCTCC	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATTC	GGCACTCGAG	CAGTCTATT	GGCCAGTGTG	GCAGCTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCCTGCTCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTCACCTTC	TCAGCCCTGC	AGATCCTGC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	1500
GAAGCAGGTG	TTCCTGCCCA	AATACCGAGG	GGACACTGGA	GGTGTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCACC	TCCACCCGCG	CTCTGCC	CCTCTGCC	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCCTGGA	TAGTGCCTTC	CTGCTGTC	AGGTGGCCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCACTGCT	ATATGGTGT	1860
TGCCGAGGC	CTGGGTCTGG	TCGCCATT	CTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCA	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGG	GGGCCTGCC	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGCTGG	GGCGTCCCTC	TCCCTCTCTC	CCAGTCTCTA	GGGCTGCC	2160
ACTGGAGGCC	TTCCAAGGGG	GTTTCAGTCT	GGACTTATAAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
TTTCTCCATC	TCTAAGCCCC	TTAACCTGCA	GCTTCGTTTA	ATGTAGCTCT	TGCA	2400
TTTCTAGGAT	AAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTG	TAGGGGAAGA	2460

GTCCCTGAGGG	GCAACACACA	AGAACCCAGGT	CCCCTCAGCC	CACAGCACTG	TCTTTTGCT	2520
GATCCACCCCC	CCTCTTACT	TTTATCAGGA	TGTGGCTGT	TGGTCCTCT	GTGCCATCA	2580
CAGAGACACA	GGCATTTAAA	TATTTAACTT	ATTTATTTAA	CAAAGTAGAA	GGGAATCCAT	2640
TGCTAGCTT	TCTGTGTTGG	TGTCTAATAT	TTGGGTAGGG	TGGGGATCC	CCAACAATCA	2700
GGTCCCCTGA	GATAGCTGGT	CATTGGGCTG	ATCATTGCCA	GAATCTTCTT	CTCCTGGGGT	2760
CTGGCCCCC	AAAATGCCTA	ACCCAGGACC	TTGGAAATT	TACTCATCCC	AAATGATAAT	2820
TCCAAATGCT	GTTACCCAAG	GTTAGGGTGT	TGAAGGAAGG	TAGAGGTGG	GGCTTCAGGT	2880
CTCAACGGCT	TCCCTAACCA	CCCCTCTTCT	CTTGGGCCAG	CCTGGTTCCC	CCCACCTCCA	2940
CTCCCCCTCA	CTCTCTCTAG	GAETGGGCTG	ATGAAGGCAC	TGCCCAAAT	TTCCCCTTAC	3000
CCCAACTTTC	CCCTACCCCC	AACTTTCCCC	ACCAGCTCCA	CAACCTGTT	TGGAGCTACT	3060
GCAGGACCAG	AAGCACAAAG	TGCGGTTTCC	CAAGCCTTG	TCCATCTCAG	CCCCCAGAGT	3120
ATATCTGTG	TTGGGAAATC	TCACACAGAA	ACTCAGGAGC	ACCCCTGCC	TGAGCTAAGG	3180
GAGGTCTTAT	CTCTCAGGGG	GGGTTTAAGT	GCCGTTTGCA	ATAATGTCGT	CTTATTATT	3240
TAGCGGGGTG	AATATTTAT	ACTGTAAGTG	AGCAATCAGA	GTATAATGTT	TATGGTGACA	3300
AAATTAAAGG	CTTTCTTATA	TGTTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3360
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAATAA	AAAAAAAAAA	AAAAAAAAAA	3410

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT	CCCTCTGCCT	GCCCACTCAG	TGGCAACACC	CGGGAGCTGT	TTTGTCTTT	60
GTGGAGCCTC	AGCAGTTCCC	TCTTTCAGAA	CTCACTGCCA	AGAGCCTGA	ACAGGAGCCA	120
CCATGCAGTG	CTTCAGCTTC	ATTAAGACCA	TGATGATCCT	CTTCATTTG	CTCATCTTTC	180
TGTGTGGTGC	AGCCCTGTTG	GCAGTGGCA	TCTGGGTGTC	AATCGATGGG	GCATCCTTTC	240
TGAAGATCTT	CGGGCCACTG	TCGTCCAGTG	CCATGCAGTT	TGTCAACGTG	GGCTACTTCC	300
TCATCGCAGC	CGGCGTTGTC	GTCTTGCTC	TTGGTTTCC	GGGCTGCTAT	GGTGCTAAGA	360
CTGAGAGCAA	GTGTGCCCTC	GTGACGTTCT	TCTTCATCC	CCTCCTCATC	TTCATTGCTG	420
AGGTTGCAGC	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCTGACGT	480
TGCTGGTAGT	GCCTGCCATC	AAGAAAGATT	ATGGTTCCCA	GGAAGACTTC	ACTCAAGTGT	540
GGAACACCAC	CATGAAAGGG	CTCAAGTGCT	GTGGCTTCAC	CAACTATAACG	GATTTTGAGG	600
ACTCACCTTA	CTTCAAAAGAG	AACAGTGCT	TTCCCCCATT	CTGTTGCAAT	GACAACGTCA	660
CCAACACAGC	CAATGAAACC	TGCACCAAGC	AAAAGGCTCA	CGACAAAAAA	GTAGAGGGTT	720
GCTTCATCA	GCTTTTGAT	GACATCCGAA	CTAATGCAGT	CACCGGGGT	GGTGTGGCAG	780
CTGGAATTGG	GGGCCTCGAG	CTGGCTGCCA	TGATTGTGTC	CATGTATCTG	TACTGCAATC	840
TACAATAAGT	CCACCTCTGC	CTCTGCCACT	ACTGCTGCCA	CATGGGAAC	GTGAAGAGGC	900
ACCCCTGGCAA	GCAGCAGTGA	TTGGGGGAGG	GGACAGGATC	TAACAATGTC	ACTTGGGCCA	960
GAATGGACCT	GCCCTTTCTG	CTCCAGACTT	GGGGCTAGAT	AGGGACCACT	CCTTTTAGCG	1020
ATGCCTGACT	TTCCTTCCAT	TGGTGGGTGG	ATGGGTGGGG	GGCATTCAG	AGCCTCTAAG	1080
GTAGCCAGTT	CTGTTGCCA	TTCCCCCAGT	CTATTAAACC	CTTGATATGC	CCCCTAGGCC	1140
TAGTGGTGAT	CCCAGTGCTC	TACTGGGGGA	TGAGAGAAAG	GCATTTTATA	GCCTGGGCAT	1200
AAGTGAATC	AGCAGAGCCT	CTGGGTGGAT	GTGTAGAAGG	CACTTCAAAA	TGCATAAAACC	1260
TGTTACAATG	TTAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1289

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
245	250	255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
260	265	270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
275	280	285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
290	295	300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala		
1	5	10
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu		
20	25	30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val		
35	40	45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly		
50	55	60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly		
65	70	75
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile		
85	90	95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu		
100	105	110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly
 115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

90

50	55	60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr		
65	70	75
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Ile Leu Leu Ile		
85	90	95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr		
100	105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys		
115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		
225	230	235
Gln		

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTCCTC TCCCCTCCTC TGAATTAAAT TCTTCAACT TGCAATTGC AAGGATTACA	60
CATTCACIG TGATGTATAAT GTGTTGCAA AAAAAAAA GTGCTTTGT TTAAAATTAC	120
TTGGTTTG TG AATCCATCTT GCTTTTCCC CATTGGAAC AGTCATTAAC CCATCTCTGA	180
ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATC TGACAGGTGA ATTGGATGGT	240
TCTCAGAACC ATTTCACCCA GACAGCCTGT TTCTATCCTG TTTAATAAAT TAGTTGGGT	300
TCTCTACATG CATAACAAAC CCTGCTCCAA TCTGTCACAT AAAAGTCTGT GACTTGAAGT	360
TTAGTC	366

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA ACCATTTCCCT ATATTATAGC AAAATTAAAA TCTACCGTA TTCTAATATT	60
GAGAAATGAG ATNAAACACA ATNTTATAAA GTCTACTTAG AGAAGATCAA GTGACCTCAA	120
AGACTTTACT ATTTTCATAT TTTAAGACAC ATGATTATC CTATTTAGT AACCTGGTTC	180
ATACGTTAAA CAAAGGATAA TGTGAACAGC AGAGAGGATT TGTTGGCAGA AAATCTATGT	240
TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCCCT TT	282

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA	60
TATTTATCCT CCCTCCTGAA ACAATTGCAA ATAANACAA AATATATGAA ACAATTGCAA	120
AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA	180
TACTGATCCC TGATCACTGT CCTAATGCGAG GATGTGGGAA ACAGATGAGG TCACCTCTGT	240
GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT	300
TGGGT	305

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTG CCGCACAAATC TGAGTGGAAA

60

AANTCCTGGG T

71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAACG GGAATTAANT
AATGGANTCA AGANACTCCC AGGCCTCAGC GT

60

120

180

212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC
CTCCGCCGGC GCAGAACATG CTGGGGTGGT

60

90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANC GTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCTAT GGTCTTTG GGAATTCCCTT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCAGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCAGG T	171

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCAATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTC ATTCTCTTGG	120
TTAAGATTTG T	131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG	60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTGGAT TAAATGAGGA TGCTGAAGAT	180
TTGCCTCACC AACACAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG	240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTGATC TGTAAGAATG GAATTGATT TGCTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAACCTC AGTGCCTCTC	420
CTCTTGCTT GT	432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACTTG AATAGTAAAA TAGAAACTGA GCTGAAATT CTAATTCACT TTCTAACCAT	60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTG ATAAAAATTG GT	112

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG	54
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(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGTCTCCCCT CTACCAGCTC	60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGCG TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGGTT ACCCATTTG GGGACCCATT ATAGGCAATA AACACAGTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTTT TCTTAGCCTT	240
TTCCTGAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTCCATG TCC	323

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTTCATC	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTTGACA	60
TATAATGACG CAACAAAAAG GTGCTTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTCCTTATTG TGTTTGCCG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTG CATTITGTTA ACGCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTTATGTGC AGCAGCTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGTGTT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCTCCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGTAAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA	240
CTTCCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA TTTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC	60
AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAAT	120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT	180
TTTAGCAAGT TAAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAAGAGTTG	240
GGATGCTTCT AAAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT	300
GTAACAACTC ACAATTGGTC CA	322

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC ACAAGTTAA CTAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT	60
CTTGTTTTC TTTCATCTG GCTCCTGGGT TGACAATTTG TGGAAACAAC TCTATTGCTA	120
CTATTAAAA AAAATCACAA ATCTTICCT TTAAGCTATG TTNAATTCAA ACTATTCCCTG	180
CTATTCCTGT TTGTCAAAG AAATTATATT TTCAAAATA TGTNTATTTG TTTGATGGGT	240
CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG	278

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GT TTANAAAA CTTGTTAGC TCCATAGAGG AAAGAATGTT AAAC TTTGTA TTTTAAAC	60
TGATTCTCTG AGGTTAAACT TG GTTTCAA ATGTTATTT TACTTGATT TTGCTTTGG	120
T	121

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC ATGCCTAGCA CATCAGAAC CCTCAAAGAA CATCAGTATA ATCC TATA ACC	60
ATANCAAGTG GTGACTGGTT AAGCGTGCAG CAAAGGTCAG CTGGCACATT ACTTGTGTGC	120
AAACTTGATA CTTTGTTC AAGTAGGAAC TAGTATACAG TNCC TAGGAN TGGTACTCCA	180
GGGTGCCCCC CAACTCCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AAC T TCGCT	240
CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTGCTGAG	300
TTCCCAAGGA TGCAAAGCCT GGTGCTAAC TCCTGGGCG TCAACTCAGT	350

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT	60
GCTGTGATTG TATCCGAATA NTCCCTGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT	120
GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCC TGCC TTGGCTCTGA	180
CCTGGCGGCC AGCCAGCCAG CCACAGGTGG CCTCTTCCT TTTGTGGTGA CAACNCCAAG	240
AAA ACTGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAAGGTGC	300
TCCCAGGAAC CGGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG	360
GGTGCAGANG GATGAAGCAG CCAGNTGTT TGCTGTGGT	399

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTTGCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGGTT CCTGT	165

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACCTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCAA	120
TGCTGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGA GGGCTGGGGG CATANANGGT	240
CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTGCCAC TGTACATTCC CCATNTTTAA	300
AAAAACTGAT GCCTTTTTT TTTTTTTTG TAAAATTC	338.

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTGGCA TCTGGTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTG CAGCCAGCCT AGTGCCGAA GTGAAGGAGA	120
ATTCAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC	180

100

ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCTGAT GTCTGTAGTT TCACAGGATG	240
CCTTATTGTT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCTACCA CTGCTGAGTG	360
GCCTGGAACT TGTTTAAAGT GT	382

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT CTTTCTGTG TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG	120
TTTTCACATT TCAACTTGTG TGTTGTTGTC TCTTANAGCA TTGGTGAAT CACATATTG	180
ATATTTCAGCA TAAAGGAGAA	200

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTTGGTGG	60
GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGTT	120
ATGCATGTAG AGAACCCAAA CTAATTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTCACTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTCTTACCC AGTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCACAAAC CAAGTAATT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA TATTGCCACA TATATCCTT CCAATTGCGG GCTAACAGA CGTGTATTTA	60
GGGTTGTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC ACAACACATC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACGTG AGCTGTTGA	360
AGCTACCACT GTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTCCCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTT GTCATTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTG TTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTTG TATTTGTAAT GGCAACATC CAGNAGCAAT TCCTAAACAA	60
ACTGGAGGGT ATTTATACCC AATTATCCC TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGT ATAAAACCTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGGAG GAAATGGAAC ATAAGCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTGAGAGA GCTCCTTGC CAACAGGCCT	120
CCAAGTCAGG GCTGGGATTT GTTCCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCTT CTGGGCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACCTT TATCTCATCG AATTTTTAAC CCAAACATCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTTCAT TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGTCTTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAATC ACCCCTTAA TTACCATGCT ATGGTGG	477

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120
GATGATAAT AAGAGTCAGC CAGGTAAGTG GGTGGGTGTT TATGGGCACA GTGAAGAACAA	180
TTTCAGGCAG AGGAAACAGC AGTAAA	207

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGGG T	111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT	120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCCTTG TGGTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGGCACTTT CACATGTAAG AAGGGAGAAA TTCTTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACAG	120
GAGGGAGTTT GT	132

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTCACTGGCC TCCAAACATG AAAGTGTCA	60
CTTCTGCTCT TATGTCCTCA TCTGACAACCT CTTTACCATTT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGCG TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCAG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCTTAAAT TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAACGCCGG TTACACAGCT AACTCCCCTGGCCTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTCAAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG	60
GAAAGTGCTT TGGGAACGTG AAAGTGCCTA ACACATGATC GATGATTGTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCCTCC TGGGCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT	240
GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGT AGGCATGCTG	300
GCCCTGGT	308

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACGTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCTTGCTT CATTCTATGT	180
CTAATATATT CTCATCAAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCCAGAT GTCTATCCTT AAGATTTCAT AATAGAAAAAC AAATTAACAG ACTAT	295

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGTA TATCTGTCCC	120
CTTAGT	126

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTCTGTGCG TGTGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCAGCCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAAGT	120
GCCTGGTAA TTCACCATTA ATTTCTTCCC CCAAACACTCTC TGAGTCTTCC CTTAATATTT	180
CTGGTGGTTC TGACCAAAGC AGGTCACTGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATGTTTGTGTA GCCTTGCATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG	300
CCAACCTGT TTTCCCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA	360
NACAGACGGG CTCTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCAATTCT CTGATGTCCT GT	442

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAC TG ATGGGTGACG TTGTAGGTTC	60
TCCAACAAGA ACTGAGGTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTT ATTCCCTACT ACGGCCAAG GTTGTGAAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGC	240
TGCTGTGGTG CGGGGANGTG AANGTGTGTT GTCACTTGAG CTTGGCCAGC TCTGGAAAGT	300
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTA	360
CGAACCCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTGN	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCA	480
AAGGAAATAA GCTGTGGT	498

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCA GATGCCTCTC	240
CCACCCCTTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTC TAACATCCTG	300
GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA	360
CTTGTAGAAT GAAGCCTGGA	380

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAAA TGATACTTAG TGAGTTTTA ATATCCTCAT ATATATCAAA	60
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT	120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACCTAC TCACGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTCT CATACTTAAT GAGGGAGTTC CAGGAGATTG AACCAGGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACGTG	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTC TACACCTGTG	240
GGTTATGACA AAGACAACTG CCAAAGAACATC TTCAAGAAGG AGGACTGCAA GTATATCGT	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTGAGC AAACACTTT	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGCGTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CGCGCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGAGG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACCTCG CCAAAGAATT	180
TTTGCAAGACC AGCCTGAGCA AGGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGGTGTC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCCTTT TTGGGTGAAC TTTC	383

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGCCCCCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAAGT TTTCTAGAAC	60
TGGAAGGATT GTANTCATCC	
TGAAAATGGG TTTACTTC	
AATCCCTCAN CCTTGTCTT CACNACTGTC	120
TATACTGANA GTGTCATGTT	
TCCACAAAGG GCTGACACCT	
GAGCCTGNAT TTTCACTCAT	180
CCCTGAGAAC CCCTTCCAG	
TAGGGTGGGC AATTCCCAAC	
TTCCCTGCCA CAAGCTTCCC	240
AGGCTTCTC CCCTGGAAAA	
CTCCAGCTG AGTCCAGAT	
ACACTCATGG GCTGCCCTGG	273
GCA	

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC	60
TCAGTGCAGA AAGATCATCT	
TCCAGCAGTC AGCTCAGACC	120
AGGGTCAAAG GATGTGACAT	
CAACAGTTTC TGTTTCAGA	
ACAGGTTCTA CTACTGTCAA	180
ATGACCCCCC ATACTTCCTC	
AAAGGCTGTG	
GTAAGTTTG CACAGGTGAG	
GGCAGCAGAA AGGGGGTANT	240
TACTGTGAA CACCATCTTC	
TCTGTATACT CCACACTGAC	
CTTGCCATGG GCAAAGGCC	300
CTACCACAAA ACAAATAGGA	
TCACTGCTGG GCACCCAGCTC	
ACGCACATCA CTGACAACCG	360
GGATGGAAAA AGAANTGCCA	
ACTTTCATAC ATCCAACCTGG	
AAAGTGATCT GATACTGGAT	420
TCTTAATTAC CTTCAAAAGC	
TTCTGGGGC CATCAGCTGC	
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA	60
TGCCTGTGCC GGCTGCTGAA	
AGGGAGTTCA GAGGTGGAGC	
TCAAGGAGCT CTGCAGGCAT	120
TTTGCCAAANC CTCTCCANAG	
CANAGGGAGC AACCTACACT	
CCCCGCTAGA AAGACACCAAG	180
ATTGGAGTCC TGGGAGGGGG	
AGTTGGGGTG GGCATTTGAT	
GTATACTTGT CACCTGAATG	240
AANGAGCCAG AGAGGAANGA	
GACGAANATG ANATTGGCCT	
TCAAAGCTAG GGGTCTGGCA	266
GGTGGAA	

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA	TCATAAACGG	CGAGGACTGC	AGCCCGCACT	CGCAGCCCTG	GCAGGGCGCA	60
CTGGTCATGG	AAAACGAATT	GTTCTGCTCG	GGCGTCTGG	TGCATCCGCA	GTGGGTGCTG	120
TCAGCCGCAC	ACTGTTTCCA	GAAGTGAGTG	CAGAGCTCT	ACACCATCGG	GCTGGGCCCTG	180
CACAGTCTTG	AGGCCGACCA	AGAGCCAGGG	AGCCAGATGG	TGGAGGCCAG	CCTCTCCGTA	240
CGGCACCCAG	AGTACAACAG	ACCCCTGCTC	GCTAACGACC	TCATGCTCAT	CAAGTTGGAC	300
GAATCCGTGT	CCGAGTCTGA	CACCATCCGG	AGCATCAGCA	TTGCTTCGCA	GTGCCCTACC	360
GCGGGGAACT	CTTGCCCTCGT	TTCTGGCTGG	GGTCTGCTGG	CGAACGGCAG	AATGCCTACC	420
GTGCTGCAGT	GCGTGAACGT	GTCGGTGGTG	TCTGAGGAGG	TCTGCAGTAA	GCTCTATGAC	480
CCGCTGTACC	ACCCCAGCAT	GTTCTGCGCC	GGCGGAGGGC	AAGACCAAGAA	GGACTCCTGC	540
AACGGTGACT	CTGGGGGGCC	CCTGATCTGC	AACGGGTACT	TGCAGGGCCT	TGTGTCTTTC	600
GGAAAAGCCC	C GTGTGGCCA	AGTTGGCGTG	CCAGGTGTCT	ACACCAACCT	CTGCAAATTC	660
ACTGAGTGGA	TAGAGAAAAC	CGTCCAGGCC	AGTTAACTCT	GGGGACTGGG	AACCCATGAA	720
ATTGACCCCC	AAATACATCC	TGCGGAAGGA	ATTCAAGGAAT	ATCTGTTCCC	AGCCCCTCCT	780
CCCTCAGGCC	CAGGAGTCCA	GGCCCCCAGC	CCCTCCTCCC	TCAAACCAAG	GGTACAGATC	840
CCCAGCCCC	CCTCCCTCAG	ACCCAGGAGT	CCAGACCCCC	CAGCCCTCC	TCCCTCAGAC	900
CCAGGAGTCC	AGCCCCCTCT	CCCTCAGACC	CAGGAGTCCA	GACCCCCCAG	CCCTCCTCC	960
CTCAGACCA	GGGGTCCAGG	CCCCCAACCC	CTCCTCCCTC	AGACTCAGAG	GTCCAAGGCC	1020
CCAACCCNTC	ATTCCCCAGA	CCCAGAGGTC	CAGGTCCCAG	CCCTCTNCC	CTCAGACCCA	1080
GCGGTCCAAT	GCCACCTAGA	CTNTCCCTGT	ACACAGTGCC	CCCTTGTGGC	ACGTTGACCC	1140
AACCTTACCA	GTTGGTTTT	CATTTTNGT	CCCTTTCCCC	TAGATCCAGA	AATAAAGTTT	1200
AAGAGAAGNG	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAA	AAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - xii) SEQUENCE DESCRIPTION: SEQ ID NO:172;

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1 5 10 15

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35 40 45

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50 55 60

Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65 70 75 80

Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
 85 90 95

Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
 100 105 110

Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
 115 120 125

Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
 130 135 140

Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC ACTCGCAGCC CTGGCAGGCG	GCAC TGGTCA TGGAAAACGA	ATTGTTCTGC	60
TCGGGCGTCC TGGTGCATCC	GCAGTGGGTG	CTGTCAGCCG	120
TACACCATCG GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	180
GTGGAGGCCA GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	240
CTCATGCTCA TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	300
ATTGCTTCGC AGTGCCTAC	CGCGGGGAAC	ACACCATCCG	360
GCGAACGGTG AGCTCACGGG	TGTGTGTCTG	GAGCATCAGC	420
CGGGGGCTGA CCCAGAGCTC	TGCGTCCCAG	TACCGTCTG	480
ACGTGTCGGT GGTGTCTGAG	GCAGAAATGCC	CAGTGCCTGA	540
GCATGTTCTG CGCCGGCGGA	GAGGTCTGCA	TGACCCGCTG	600
GGCCCCCTGAT CTGCAACGGG	GTAAGCTCTA	TACCACCCCA	660
GCCAAGTTGG CGTGCCAGGT	TACTTGAGG	CTGCAACGGT	720
	GCCTTGTGTC	GACTCTGGGG	
	TTTCGGAAAA	GCCCCGTGTG	
	ATTCACTGAG	TGGATAGAGA	

AAACCGTCCA	G GCCAGTTAA	C T C T G G G A C	T G G G A A C C A	T G A A A T T G A C	C C C C A A A T A C	780
A T C C T G C G G A	A G G A A T T C A G	G A A T A T C T G T	T C C C A G C C C C	T C C T C C C T C A	G G C C C A G G A G	840
T C C A G G C C C C	C A G C C C C T C C	T C C C T C A A A C	C A A G G G T A C A	G A T C C C C A G C	C C C T C C T C C C	900
T C A G A C C C A G	G A G T C C A G A C	C C C C C A G G C C	C T C C T C C C T C	A G A C C C A G G A	G T C C A G G C C C C	960
T C C T C C N T C A	G A C C C A G G A G	T C C A G A C C C C	C C A G G C C C T C	C T C C T C A G A	C C C A G G G G T T	1020
G A G G C C C C C A	A C C C C T C C T C	C T T C A G A G T C	A G A G G T C C A A	G C C C C C A A C C	C C T C G T T C C C	1080
C A G A C C A G A G	G G T N N A G G T C	C C A G C C C T C	T T C C N T C A G A	C C C A G N G G T C	C A A T G C C A C C	1140
T A G A T T T C C	C T G N A C A C A G	T G C C C C T T G	T G G N A N G T T G	A C C C A A C C T T	A C C A G T T G G T	1200
T T T C A T T T T	T N G T C C C T T T	C C C C T A G A T C	C A G A A A T A A A A	G T T T A A G A G A	N G N G C A A A A A	1260
AAAAAA						1265

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

G G T C A G C C G C	A C A C T G T T T C	C A G A A G T G A G	T G C A G A G G C T C	C T A C A C C A T C	G G G C T G G G C C	60
T G C A C A G T C T	T G A G G C C G A C	C A A G A G C C A G	G G A G G C C A G A T	G G T G G A G G G C C	A G C C T C T C C G	120
T A C G G C A C C C	A G A G T A C A A C	A G A C C C T T G C	T C G C T A A C G A	C C T C A T G C T C	A T C A A G T T G G	180
A C G A A T C C G T	G T C C G A G T C T	G A C A C C A T C C	G G A G C A T C A G	C A T T G C T T C G	C A G T G C C C T A	240
C C G C G G G A A	C T C T T G C C T C	G T T T C T G G C T	G G G G T C T G C T	G G C G A A C G G T	G A G C T C A C G G	300
G T G T G T G T C T	G C C C T C T T C A	A G G A G G T C C T	C T G C C C A G T C	G C G G G G G C T G	A C C C A G A G G C T	360
C T G C G T C C A	G G C A G A T G C	C T A C C G T G C T	G C A G T G C G T G	A A C G T G T C G G	T G G T G T C T G A	420
N G A G G T C T G C	A N T A A G C T C T	A T G A C C C G C T	G T A C C A C C C C	A N C A T G T T C T	G C G C C G G C G G	480
A G G G C A A G A C	C A G A A G G A C T	C C T G C A A C G T	G A G A G A G G G G	A A A G G G G A G G	G C A G G C G A C T	540
C A G G G A A G G G	T G G A G A A G G G	G G A G A C A G A G	A C A C A C A G G G	C C G C A T G G C G	A G A T G C A G A G	600
A T G G A G A G A C	A C A C A G G G A G	A C A G T G A C A A	C T A G A G A G A G	A A A C T G A G A G	A A A C A G A G A A	660
A T A A A C A C A G	G A A T A A A G A G	A A G C A A A G G A	A G A G A G A A A C	A G A A A C A G A C	A T G G G G A G G C	720
A G A A A C A C A C	A C A C A T A G A A	A T G C A G T T G A	C C T T C C A A C A	G C A T G G G G C C	T G A G G G C G G T	780
G A C C T C C A C C	C A A T A G A A A A	T C C T C T T A T A	A C T T T G A C T	C C C C A A A A A C	C T G A C T A G A A	840
A T A G C C T A C T	G T T G A C G G G G	A G C C T T A C C A	A T A A C A T A A A	T A G T C G A T T T	A T G C A T A C G T	900
T T T A T G C A T T	C A T G A T A T A C	C T T T G T T G G A	A T T T T T G A T	A T T T C T A A G C	T A C A C A G T T C	960
G T C T G T G A A T	T T T T T T A A A A T	T G T T G C A A C T	C T C C T A A A A T	T T T T C T G A T G	T G T T T A T T G A	1020
A A A A A T C C A A	G T A T A A G T G G	A C T T G T G C A T	T C A A A C C A G G	G T T G T T C A A G	G G T C A A C T G T	1080
G T A C C C A G A G	G G A A A C A G T G	A C A C A G A T T C	A T A G A G G T G A	A A C A C G A A G A	G A A A C A G G A A	1140
A A A T C A A G A C	T C T A C A A A G A	G G C T G G G C A G	G G T G G G C T A T	G C C T G T A A T C	C C A G C A C T T T	1200
G G G A G G C G A G	G C A G G C A G A T	C A C T T G A G G T	A A G G A G T T C A	A G A C C A G C C T	G G C C A A A A T G	1260
G T G A A A T C C T	G T C T G T A C T A	A A A A T A C A A A	A G T T A G C T G G	A T A T G G T G G C	A G G C G C C T G T	1320
A A T C C C A G C T	A C T T G G G A G G	C T G A G G C A G G	A G A A T T G C T T	G A A T A T G G G A	G G C A G A G G T T	1380
G A A G T G A G T T	G A G A T C A C A C	C A C T A T A C T C	C A G C T G G G G C	A A C A G A G T A A	G A C T C T G T C T	1440
C A A A A A A A A A A	A A A A A A A A A A					1459

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCAGCCCT	GGCAGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGCGTCCCTG	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTCC	AGAACTCCTA	CACCATCGGG	120
CTGGGCTCTG	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGGA	GCCAGATGGT	GGAGGCCAGC	180
CTCTCCGTAC	GGCACCCCAGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGITGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGCAG	300
TGCCCTACCG	CGGGGAACTC	TTGCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360
ATGCCTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGANGT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480
GACTCCTGCA	ACGGTGACTC	TGGGGGGCCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540
GTGTCTTTCG	GAAAAGCCCC	GTGTGGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600
TGCAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATAACATCCT	GCGGAANGAA	TTCAGGAATA	TCTGTTCCCA	720
GCCCCCTCCTC	CCTCAGGCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTCNT	840
CCNTCAGACC	CAGGAGTCCA	GCCCCTCCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCNTCCNTCA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAAGC	CCCTCCTCCC	1020
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCCC	CCTTGTGGCA	1080
NGTTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTC	CCTTTCCCT	AGATCCAGAA	1140
ATAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10			15			

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
							20		25				30		

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Leu	Leu	Leu
50															60
Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
65															80
Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
															95
Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met
															110
Pro	Thr	Val	Leu	His	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Xaa	Val
															125
Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala
															140
Gly	Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly
145															160
Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys
															175
Ala	Pro	Cys	Gly	Gln	Leu	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys
															190
Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Xaa	Ser			
															205

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GGCGGCACTG	GTCATGGAAA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGAGTG	GGTGTGTCA	GCCGACACT	GTTTCCAGAA	CTCCTACACC	120
ATCGGCTGG	GCCTGCACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCCAGCCTCT	CCGTACGGCA	CCCAGAGTAC	AACAGACCCCT	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGCAGTGCC	CTACCGCGGG	GAACTCTTGC	CTCGTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATGCTGTGA	TTGCCATCCA	GTCCCAGACT	GTGGGAGGCT	GGGAGTGTGA	GAAGCTTCC	420
CAACCCTGGC	AGGGTTGTAC	CATTTGGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480

CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG	540
CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGCTTATTGT	600
ACTAACCATG CCGATGTTA GGTGAAATTA GCGTCACTTG GCCTCAACCA TCTTGGTATC	660
CAGTTATCCT CACTGAATTG AGATTCCTG CTTCAAGTGC AGCCATTCCC ACATAATTTC	720
TGACCTACAG AGGTGAGGGG TCATATAGCT CTTCAAGGAT GCTGGTACTC CCCTCACAAA	780
TTCATTTCTC CTGTTGAGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCCAGGG TGGGTGTGCA	840
GGTCACAATG ATGAATGTAT GATCGTGTTC CCATTACCCA AAGCCTTAA ATCCCTCATG	900
CTCAGTACAC CAGGGCAGGT CTAGCATTTC TTCATTTAGT GTATGCTGTC CATTGATGCA	960
ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCTGGG	1020
GAGGTGAGGG AGAGGGCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC	1080
TTAATAAACAA GAAGCTGTGA TGTAAAAAAA AAAAAAAA	1119

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp			
1	5	10	15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu		
20	25	30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val		
35	40	45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu		
50	55	60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser		
65	70	75

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly		
85	90	95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val		
100	105	110

Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu		
115	120	125

Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg		
130	135	140

Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser	
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145

150

155

160

Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCCTTTC AAGCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCCCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGGC TGTGATTGCT	120
GCCAGGCACT GTTCATCTCA GCTTTCTGT CCCTTGCTC CCGGCAAGCG CTTCTGCTGA	180
AAGTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAAA	240
AAAAAAAAAAA	250

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACCA	60
TCACCCAGAC CCCGCCCCCTG CCCGTGCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA	120
CTCTGCTACT CGGAAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGTT TATAAATGCC	180
TGATTTAAAA AAAAAAAAAAA AA	202

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG	60
AATGTTTAGG CAGTGCTAGT AATTTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT	120
TTATTCCTCT TTCTTCTGAA GATTAATGAA GTTAAAATT GAGGTGGATA AATACAAAAA	180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA	240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC	300
CTACTCTGTT CCTGGCTAG AAAAAATTAT AACACAGGACT TTGTTAGTTT GGGAGCCAA	360
ATTGATAATA TTCTATGTTA TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW	420

TTTTATTCCC AGGAATATGG KGTTCATTTT ATGAATATTA CSCRGGATAG AWGTWTGAGT	480
AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACITTATTTC	540
CAAAAAAAA AAAAAAAA	558

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCCRGA RWTYGTTGA TCCAACCCTG GCTTWTTTTC	60
AGAGGGAAA ATGGGGCCTA GAAGTACAG MSCATYTAGY TGGTGCAGTG GCACCCCTGG	120
CSTCACACAG ASTCCCGAGT AGCTGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG	180
TTWGCAATTAC CGTTGCCAC CTCCAACCTA AACATTCTTC ATATGTGATG TCCTTAGTCA	240
CTAAGGTTAA ACTTTCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA	300
TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGTT GATAGGAANT	360
NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTG TACGCATARA	420
AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAA AAAAAAAA	479

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC AGAACGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAG TGCCAGTGCC AGTGCAGCA CCAGTGGTGG CTTCAGTGCT	120
GGTGCAGCC TGACCGCCAC TCTCACATT GGCTCTTCG CTGGCCCTGG TGGAGCTGGT	180
GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTTCTCCT ACAAGTGAGA TTTTAGATAT	240
TGTTAACCTC GCCAGTCTTT CTCTTCAGC CAGGGTGAC CCTCAGAAC CTAACCAACA	300
CAGCACTCTA GGCAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATT	360
GCCATTCAA AAAAAAAA AAAA	384

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYYNT CCRGTATKAC CTCAACGAGC	60
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120

AGGGAGATCG AGTCTATAACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG	120
CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAAC ACCATCAAGA	180
AACGCTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC	240
TGATGTCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAACCT CTTCGGACTG	300
TGAGCCCTGA TGCCCTTTTG CCAGCCATAC TCTTGGCAT CCAGTCTCTC GTGGCGATTG	360
ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCCATA AAGGAAACAC ATTTGACTTT	420
TTTTCTCAT ATTTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWTT GAAAAACTST	480
TAAAAAAAAA AAAAAA	496

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC	60
CAAGTATCYT GCGCSGCGTC TTCTACCGTC CCTACCTGCA GATCTCGGG CAGATTCCCC	120
AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAACTG YTCGTCGGAG CCCGGCTTCT	180
GGGCACACCC TCCTGGGGCC CAGGCGGGCA CCTGCGTCTC CCAGTATGCC AACTGGCTGG	240
TGGTGTGCT CCTCGTCATC TTCCCTGCTCG TGGCCAACAT CCTGCTGGTC AACTTGCTCA	300
TTGCCATGTT CAGTTACACA TTGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG	360
GCGCAGCGTT ACCGCCTCAT CCGG	384

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC CTCCACAAACC TTGATGAGGT CGTCTGCAGT GGCTCTCGC TTCATACCGC	60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGCG GCNTAATATT	120
CCAGGAAACT CTCATCAAG TCACCGTCGA TGAAACCTGT GGGCTGGTTC TGTCTTCCGC	180
TCGGTGTGAA AGGATCTCCC AGAAGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT	240
ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACCAAG CTCTCTGACA GTGAGGTAC	300
CAGCCCTATC ATGCCGTTGA MCGTGCGAA GARCACCGAG CCTTGTTGGGG KKKGKAAGT	360
CTCACCCAGA TTCTGCATTA CCAGAGAGGCC GTGGCAAAG ACATTGACAA ACTCGCCAG	420
GTGGAAAAG AMCAMCTCCT GGARGTGCTN GCGCCTCCTC GTCMGTGGT GGCAGCGCTW	480
TCCTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCC CCAGAAANTT GTCATCATCC	540
AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAAT	577

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGSTG AGAATYCATW	60
ACTKGAAAAA GMAACATTAA AGCCTGGACA CTGGTATTAA AATTCAACAT ATGCAACACT	120
TTAACACAGTG TGTCAATCTG CTCCCCYNAC TTTGTCATCA CCAGCTCTGGG AAKAAGGGTA	180
TGCCCTATTAC ACACCTGTAA AAAGGGCGCT AAGCATTTT GATTCAACAT CTTTTTTTTT	240
GACACAAGTC CGAAAAAAAGC AAAAGTAAAC AGTTATYAAAT TTGTTAGCCA ATTCACTTTC	300
TTCATGGGAC AGAGCCATTG GATTAAAAAA GCAAATTGCA TAATATTGAG CTTYGGGAGC	360
TGATATTGAGA GCGGAAGAGT AGCCTTTCTA CTTCACCAGA CACAACCTCCC TTTCATATTG	420
GGATGTTNAC NAAAGTWATG TCTCTWACAG ATGGGATGCT TTTGTGGCAA TTCTGTTCTG	480
AGGATCTCCC AGTTTATTAA CCACCTGCAC AAGAAGGCGT TTCTCCCTC AGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCACT ATCTCTAAA ACAACCTCTC ATACCTTGTG GACCTAATTG TGTGTGGTG	60
TGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTGTA AAAGCTTATG	120
CCTCTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGTCTTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTC TCTAGTTNGT	240
TTTATTCGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTKGACKARG	300
GGGGACAAAG AAAAGCAAAA CTGAMCATAA RAAACAATWA CCTGGTGAGA ARTTGATCAA	360
ACAGAAATWR GTAGTATAT TGAARNACAG CATCATTAAA RMGTTWTKTT WTTCTCCCTT	420
GCAAAAAACA TGTACNGACT TCCCGTTGAG TAATGCCAG TTGTTTTTT TATNATAAAA	480
CTTGCCTTC ATTACATGTT TNAAAGTGGT GTGGTGGGCC AAAATATTGA AATGATGGAA	540
CTGACTGATA AAGCTGTACA AATAAGCAGT GTGCCTAACCA AGCAACACAG TAATGTTGAC	600
ATGCTTAATT CACAAATGCT AATTCTATTA TAAATGTTG CTAAAATACA CTTTGAACTA	660
TTTTTCTGTN TTCCAGAGC TGAGATNTTA GATTTATGT AGTATNAAGT GAAAANTAC	720
GAAAATAATA ACATTGAAGA AAAANANAAA AAANAAAAAA A	761

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTT TTTGCCGATN CTACTATTTT ATTGCAGGAN GTGGGGGTGT ATGCACCGCA	60
CACCGGGGCT ATNAGAAGCA AGAAGGAAGG AGGGAGGGCA CAGCCCTTG CTGAGCAACA	120
AAGCCGCCTG CTGCCCTCTC TGTCTGTCTC CTGGTGCAGG CACATGGGA GACCTTCCCC	180

AAGGCAGGGG	CCACCAAGTCC	AGGGGTGGGA	ATACAGGGGG	TGGGANGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTGC	CCTGCCAGG	CACAGCGTAN	ATCTGGAAA	GACAGAATGC	TTTCCTTTTC	360
AAATTTGGCT	NGTCATNGAA	NGGGCANTTT	TCCAANTING	GCTNGGTCTT	GGTACNCTTG	420
GTTCGGCCA	GCTCCNCCTC	AAAAAANTAT	TCACCCNNCT	CCNAATTGCT	TGCNGGNCCC	480
CC						482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT	TTTTAAAACA	GTCCCCACCA	ACAAAATTAA	TTAGAAGAAT	AGTGGTTTTG	60
AAAACCTCTCG	CATCCAGTGA	GAACCTACCAT	ACACCACATT	ACAGCTNGGA	ATGTNCTCCA	120
AATGTCTGGT	CAAATGATAC	AATGGAACCA	TTCAATCTTA	CACATGCACG	AAAGAACAAAG	180
CGCTTTGAC	ATACAATGCA	CAAAAAAAA	AGGGGGGGGG	GACCACATGG	ATTAAAATTT	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTCNAAAATC	AGAACTGCNT	300
TGAAAAAATT	CATGTATGCA	ATCCAACCAA	AGAACTTNAT	TGGTGATCAT	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNAA	ANCACNCNGT	ACAAAAANAA	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATNTTNNT	TATACACTCC	C	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTT	TASTGTCGGM	CTGTTCAGCC	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACTGTCTGT	AAGCTTTTA	ACCCAGACWG	TATCTTCATA	AATAGAACAA	120
ATTCTTCACC	AGTCACATCT	TCTAGGACCT	TTTTGGATTC	AGTTAGTATA	AGCTCTTCCA	180
CTTCCTTTGT	TAAGACTTCA	TCTGGTAAAG	TCTTAAGTTT	TGTAGAAAGG	AATTYAATTG	240
CTCGTTCTCT	AAACATGTCC	TCTCCTTGAA	GTATTTGGCT	GAACAAACCA	CCTAAAGTCC	300
CTTGTGCT	CCATTTAAA	TATACTTAAT	AGGGCATTGK	TNCACTAGGT	TAATTCTGC	360
AAGAGTCATC	TGTCTGCAA	AGTTGCGTTA	GTATATCTGC	CA		402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCYTYTTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAACACACYT	CCATCCCGYT	180
CTTTGTGGA	AAAAGTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCAACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCATT	GCTTTTGTC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTGTTT	CAAAGCARC	TCTTGGTGCC	420
TGTTGGATCA	GGTTCCCAATT	TCCCAGTCYG	AATGTTACA	TGGCATATT	WACTTCCAC	480
AAAACATTGC	GATTTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAGCA	600
G						601

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCA	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GAECTCTCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAACCTCAY	TCGTGGCTTG	GGGTKGACGG	180
TKAAGTGCAG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAG	GATGCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCCCAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCAGTG	TGTCGCGCTC	420
CAGGAMMGSC	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTGCGCCTG	CGTGAGCAGC	ATGAAGGCAGT	TGTGGCTCG	CAGTTCTTCT	TCAGGAACTC	600
CACGCAAT						608

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCACAAAC	240
AAACAACAACA	AAATAACATG	TTTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTC	TGTATTATT	GKTNCTSTGG	360
AAATAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTC	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAGGC	CCCATTCCGG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCCTCTCA	GTCCCCCTCC	STACACCCCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGGAR	TGTGCTCAAG	GARTCGCNNG	420
GCARCGTGG	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAA	AAAAANAAAA	AA				502

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATT	120
WAGCTGTTK	GAGTTGATT	GCACCACTGC	ACCCACA	TCAATATGAA	AACYAWTTGA	180
ACTWATTAT	TATCTTGTA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTAAATTAT	GATTGCCATT	300
ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTCACAGT	AATATATGCC	TTTTGTAAC	360
TCACITGGTT	ATTTTATTGT	AAATGARTTA	CAAAATTCTT	AATTTAAGAR	AATGGTATGT	420
WATATTTATT	TCATTAATT	CTTCCCTKGT	TTACGTWAAT	TTGAAAAGA	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTG	ACCCACATCC	CTATGAGTT	540
TTCTTACAAT	GTATAAAAGGT	TGTAGCCAT	CNAACTTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGCAATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAAN	660
	AAGTG					665

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTT	TTTTTTTG	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTATAA	NATTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAT	CAAACATGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGTAC	300
ATTCTCTTCT	GAACTTAGA	TTTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNNTTTGN	ATTCANTCCT	GTANNAANTA	TTTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAAT	240
NATATATGTC	AATCNGATT	AAGATACAAA	ACAGATCTTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGAATTGT	CCTCCAACAA	AACCCCTG	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGAATTCA	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAAAT	ACCACATGTN	TGTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCTT	GCTCCTCTGC	480
GA						482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCAGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGGC GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCCTCGGGGA	180
CAGCCGGAAC AGAGCCCGGT GAANGCGGGA GGCCTCGGGG AGCCCTCGG GAAGGGCGGC	240
CCGAGAGATA CGCAGGTGCA GGTGGCCGCC	270

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT TTTTGGAAATC TACTGGCAGGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCAAG GTCAACTTCC TTTGTCGTGG	120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAANCGAACG ANAANTAAACA	180
TGGAGTGGGT GCACCCCTCCC TGTAGAACCT GGTTACNAAA GCTTGGGCA GTTCACCTGG	240
TCTGTGACCG TCATTTTCTT GACATCAATG TTATTAGAAG TCAGGATATC TTTTAGAGAG	300
TCCACTGTNT CTGGAGGGAG ATTAGGGTTT CTTGCCAANA TCCAANCAAA ATCCACNTGA	360
AAAAGTTGGA TGATNCANGT ACNGAATACC GANGGCATAN TTCTCATANT CGGTGGCCA	419

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	60
TGGCACTTAA TCCATTTTA TTTCAAATG TCTACAAANT TTNAATNCNC CATTATACNG	120
GTNATTTNC AAAATCTAAA NNTTATTCAA ATNTNAGCCA AANTCCTTAC NCAAAATNNAA	180
TACNCNAAA AATCAAAAAT ATACNTNTCT TTCAGCAAAC TTNGTTACAT AAATTAAAAA	240
AATATATACG GCTGGTGTGTT TCAAAGTACA ATTATCTAA CACTGCAAAC ATNTTTNNAA	300
GGAACCTAAA TAAAAAAAAA CACTNCCGCA AAGGTTAAAG GGAACAAACAA ATTCTNTTTA	360
CAACANCNC NATTATAAAA ATCATATCTC AAATCTTAGG GGAATATATA CTTCACACNG	420
GGATCTAAC TTTTACTNCA CTTTGTGTTAT TTTTTTANAA CCATTGTNTT GGGCCCAACA	480
CAATGGNAAT NCCNCCNCNC TGGACTAGT	509

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTGTG	CCCCCTCTT	ATAAAAACA	AGTTACCAATT	TTATTTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATTC	TTAGGAATTA	GCTTAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAAAC	ATCCAAATTC	240
ATTTTTCTTG	TCTTTAAAAT	TATCTAATCT	TTCCATTTT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATTTC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAA	360
AGGGAAAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTGAAGCC	AGCTAAAAG	AAGGCTTAGA	TCCTTTTATG	480
TCCATTTTAG	TCACTAAACG	ATATCNAAAAG	TGCCAGAATG	CAAAAGGTTT	GTGAACATT	540
ATTCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTT	CTG		583

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTNCTC	TTCTTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATCTTC	CAGCTTAAA	120
AATCTCTTAT	GCTATATCAT	ATTTAAGTT	AAACTAATGA	GTCACTGGCT	180
TGAAGGAAAT	CTGTTCATTC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	240
TGAGAGGTTT	TTCTTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTA	300
ATTTCATGC	AAACTAGAAA	ATAATGNTT	CTTTTGATCA	TCAAACCTT	360
CATTACAAAA	CTGCTCAAAT	TGTTTGTAA	GNTTATCCAT	TATAATTAGT	420
CTAACACAAA	TCACATTTAC	NGACNAGCAA	TAATAAAAAC	GAAGTACCA	480
AAAATAATT	AAGGAACATT	TTTGCCTGG	GTATAATTAG	TTAAATATCC	540
TTATTNAGAA	TGAATTCA	TGTTATTATT	CCNTAGCCC	ACACAATGG	589

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTNTTTT	TTTTTCAGT	AATAATCAGA	ACAATATTAA	TTTTTATATT	TAAAATTCCAT	60
AGAAAAGTGC	CTTACATTAA	ATAAAAGTTT	GTTTCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AATTTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTAAAAGA	TAAAATTGTA	CCTCAGAAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAAA	AAAATTACTA	TGGACTTCTT	GCTTTAATT	TGTGATGAAT	300
ATGGGGTGTG	ACTGGTAAAC	CAACACATTC	TGAAGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTACTTT	GCTANATNAC	GTGGATATGA	GTTGACAAGT	TTCTCTTTCT	TCAATCTTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTTC	TTTCTATNGG	480
AAGGATTAGA	TATGTTTCTT	TTGCCAATAT	AAAAAAAATA	ATAATGTTA	CTACTAGTGA	540
AACCC						545

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT	TTTTTTAGTC	AAGTTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATTT	60
CATTATTAG	CTCTGCACT	TACATATTAA	AATTAAAGAA	ACGTTNTTAG	ACAACGTINA	120
CAATTATAAA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGCAA	ACGCTAAATC	TCTTCTCCAT	CCCCATGTNG	ATATTGTGTA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAT	CAACAGCAAG	ATGAAGCTAG	GCNTGGGCTT	360
TCGGTAAAAA	TAGACTGTGT	CTGCTGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCGCTTCCT	CAAAGGCNGC	TGCCACATTT	GTGGCNTCTN	TTGCACTTGT	480
TTCAAAA						487

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTANAA	CTAGCAACTC	TTATTTCTTT	CCTTTAAAAA	60
TACATAGCAT	TAAATCCAA	ATCCTATTAA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCATTTATAG	GACCTTCTGG	TGGTTCTGCT	GTTACNTTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTGCAT	GCAGAGGAGG	AAAAAGGTAT	TGGATTTC	CAGAGGAANA	ACACAGCGCA	240
GAAATGAAGG	GGCCAGGCTT	ACTGAGCTTG	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300
AAAAGAAGGC	AGCCTAGGCC	CTGGGGAGCC	CA			332

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GCGGAGGGCG	TTACTGTTT	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTTGTGTTCC	GGCCCCATCC	AACCACGAAG	TTGATTCTC	TTGTGTGCAG	AGTGACTGAT	120
TTTAAAGGAC	ATGGAGCTTG	TCACAATGTC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCCGCGTGA	TTCACATTTA	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAAATACT	240
TTTGGCAGAA	TACTTNTGTA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTTCCCAA	300
GTAAATAGAA	GTGGGTCTATA	ATATTAATTA	CCTGTTACAA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCCAG	ACACTGACAT	CAAACTAAGC	CCACTTAGAC	TCCTCACCAC	CAGTCTGTCC	420
TGTCATCAGA	CAGGAGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCAATC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCGGTAATG	CACCACCTTG	GTGA		524

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA	ATCCAGAGTT	GCCATGGAGA	AAATTCCAGT	GTCAGCATTG	TTGCTCCTTG	60
TGGCCCTCTC	CTACACTCTG	GCCAGAGATA	CCACAGTCAA	ACCTGGAGCC	AAAAAGGACA	120
CAAAGGACTC	TCGACCCAAA	CTGCCCCAGA	CCCTCTCCA			159

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC	AGACAAAGGC	AGAGGGAGAGA	GCTCTGTTAG	TTCTGTGTTG	TTGAAC TGCC	60
ACTGAATTTC	TTTCCACTTG	GACTATTACA	TGCCANTTGA	GGGACTAATG	GAAAAACGTA	120
TGGGGAGATT	TTANCCAATT	TANGTNTGTA	AATGGGGAGA	CTGGGGCAGG	CGGGAGAGAT	180
TTGCAGGGTG	NAAATGGGAN	GGCTGGTTTG	TTANATGAAC	AGGGACATAG	GAGGTAGGCA	240
CCAGGATGCT	AAATCA					256

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTT	TTTGAGATAA	AGCATTGAGA	GAGCTCTCCT	TAACGTGACA	CAATGGAAGG	60
ACTGGAACAC	ATACCCACAT	CTTGTTCCTG	AGGGATAATT	TTCTGATAAA	GTCCTGCTGT	120
ATATTCAAGC	ACATATGTTA	TATATTATTC	AGTCCATGT	TTATAGCCTA	GTAAAGGAGA	180
GGGGAGATAC	ATTNGAAAG	AGGACTGAAA	GAAATACTCA	AGTNGGAAAA	CAGAAAAAGA	240
AAAAAAGGAG	CAAATGAGAA	GCCT				264

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT	CCAATGCTGA	ATATTTGGCT	TCATTATTCC	CANATTCTTT	GATTGTCAAA	60
GGATTTAACG	TTGTCTCAGC	TTGGGCACCT	CAGTTAGGAC	CTAAGGATGC	CAGCCGGCAG	120
GTTTATATAT	GCAGCAACAA	TATTCAAGCG	CGACAAACAGG	TTATTGAACT	TGCCCGCCAG	180
TTNAATTTC	TTCCCATTGA	CTTGGGATCC	TTATCATCAG	CCAGAGAGAT	TGAAAATTAA	240
CCCCTACNAC	TCTTTACTCT	CTGGANAGGG	CCAGTGGTGG	TAGCTATAAG	CTTGGCCACA	300
TTTTTTTTTC	CTTTATTCC	TTGTCAGA				328

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC	AGAGCGACAT	ATCCNAGTGT	AGACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAANC	CATGTTAANA	AACAAATATC	TCTCTNACCT	240
TCTCATCGGT						250

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAAC	TC	CAATGCTGAA	TATTTGGCTT	CATTATTCCC	AGATTCTTG	ATTGTCAAAG	60
GATTTAATGT	TGTCTCAGCT	TGGGCACCTTC	AGTTAGGACC	TAAGGATGCC	AGCCGGCAGG	120	
TTTATATATG	CAGCAACAAT	ATTCAGCGC	GACAACAGGT	TATTGAACCTT	GCCCCGCCAGT	180	
TGAATTTCAT	TCCCATTGAC	TTGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTAC	240	
CCCTACGACT	CTTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCCACAT	300	
TTTTTTTCC	TTTATTCCCTT	TGTCAGAGAT	GCGATTCAATC	CATATGCTAN	AAACCAACAG	360	
AGTGACTTTT	ACAAAATTCC	TATAGANATT	GTGAATAAAA	CCTTACCTAT	AGTTGCCATT	420	
ACTTTGCTCT	CCCTAATATA	CCTC				444	

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCGACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTCAAT	TCTCCAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAAGC	CATGTTGAGA	AACAAATATC	TCTCTGACCT	240
TCTCATCGGT	AAGCAGAGGC	TGTAGGCAAC	ATGGACCATA	GCGAANAAAAA	AACTTAGTAA	300
TCCAAGCTGT	TTTCTACACT	GTAACCAGGT	TTCCAACCAA	GGTGGAAATC	TCCTATACTT	360
GGTGCC						366

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC	AGAAACTCCAC	TGCANGAGGG	AGGGCCGGGC	CAGGAGAATC	TCCGCTTGTC	60
CAAGACAGGG	GCCTAAGGAG	GGTCTCCACA	CTGCTNNTAA	GGGCTNTTNC	ATTTTTTAT	120
TAATAAAAAG	TNNAAAAGGC	CTCTTCTCAA	CTTTTTTCCC	TTNGGCTGGA	AAATTTAAA	180
ATCAAAAATT	TCCTNAAGTT	NTCAAGCTAT	CATATATACT	NTATCCTGAA	AAAGCAACAT	240

AATTCTTCCT TCCCTCCTTT

260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCCTAT AATTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGAA GGACAGCACT GAAAAATT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCTA	240
ATATCCTTCA TGCTTGTAAA GT	262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNNA NGTCCAGGGT TGCTAGGAA	180
ANAAAATCAGC AGACACAGGT GTAAA	205

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCAC AATATTTGTC GATATTCCCT TCATCTTGGA TTCCATGAGG	60
TCTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTTCTTCACC TGTCCCCCAA TCCTTAAAGG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAAATAA TGAATTTTTG CATAATCCAA	180
TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGAAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTTACA TATATCTGGC ATATTGAGT	300
CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T	351

(2) INFORMATION FOR SEQ ID NO:223

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA ACAAAAAAA ACAATTCTTC ATTCAAGAAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTAA ATWRTRTTK GTGGCATTTC CTTACATTGT CTTGACAAGA	120
TTAAAATGTC TGTGCCAAA TTTTGTATTT TATTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT	240
TAAAAGATTT TGATTTCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTTTG	360
ACCATTAAGC TATATGTTA AAA	383

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCCTGAAGG CTTCTTGTAA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTCTCR AAATGGAAGC CCTTAAAGGT GCTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:
 - (a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
 - (b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.
2. The method of claim 1 wherein the binding agent is a monoclonal antibody.
3. The method of claim 2 wherein the binding agent is a polyclonal antibody.
4. A method for monitoring the progression of prostate cancer in a patient, comprising:
 - (a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;
 - (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;
 - (c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.